GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 14:48:45 ; Search time 3856 Seconds
                                            (without alignments)
                                    10078.082 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg..........tggctgcgtacttcgccagc 802

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size :   19

Total number of hits satisfying chosen parameters: 197

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   GenEmbl:*
                  1: gb_ba:*
                  2: gb_htg:*
                  3: gb_in:*
                  4: gb_om:*
                  5: gb_ov:*
                  6: gb_pat:*
                  7: gb_ph:*
                  8: gb_pl:*
                  9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                        %
Result   Query
   No.   Score Match Length DB   ID   Description
----
      1   802 100.0   802 6   AX513136   AX513136 Sequence
      2   802 100.0 327650 1   BX248337   BX248337 Mycobacte
      3   802 100.0 349306 1   BX842575   BX842575 Mycobacte
      4   751   93.6 110000 1   AE000516_10   Continuation (11 o

5	577	71.9	628	6	AX513137	AX513137	Sequence
6	369	46.0	369	6	BD171700	BD171700	Identific
7	302	37.7	323	6	BD171699	BD171699	Identific
8	196	24.4	1058	6	AR169193	AR169193	Sequence
9	196	24.4	1058	6	BD205858	BD205858	Compounds
10	196	24.4	1058	6	CQ785444	CQ785444	Sequence
11	196	24.4	1058	6	AR182483	AR182483	Sequence
12	196	24.4	1058	6	AR194866	AR194866	Sequence
13	196	24.4	1058	6	AR233138	AR233138	Sequence
14	196	24.4	1058	6	AR353343	AR353343	Sequence
15	196	24.4	1058	6	AX429637	AX429637	Sequence
16	196	24.4	1058	6	AX832622	AX832622	Sequence
17	196	24.4	1058	6	BD006366	BD006366	Compounds
18	196	24.4	1058	6	BD006486	BD006486	Compounds
19	196	24.4	1058	6	BD069326	BD069326	Compounds
20	194	24.2	611	6	BD171688	BD171688	Identific
21	159	19.8	611	6	BD171689	BD171689	Identific
22	46	5.7	712	6	AX513135	AX513135	Sequence
23	31	3.9	745	6	AX513131	AX513131	Sequence
24	30	3.7	594	6	BD171693	BD171693	Identific
25	30	3.7	785	6	AX513132	AX513132	Sequence
26	29	3.6	625	6	BD171692	BD171692	Identific
27	29	3.6	642	6	AX513130	AX513130	Sequence
28	26	3.2	533	6	BD171695	BD171695	Identific
29	26	3.2	690	6	BD171684	BD171684	Identific
30	26	3.2	690	6	BD171685	BD171685	Identific
31	26	3.2	691	6	AX513133	AX513133	Sequence
32	26	3.2	698	6	AX513134	AX513134	Sequence
33	26	3.2	707	6	AX513139	AX513139	Sequence
34	26	3.2	724	6	BD171686	BD171686	Identific
35	26	3.2	731	6	BD171687	BD171687	Identific
36	26	3.2	881	6	AX513129	AX513129	Sequence
37	26	3.2	1832	1	MP34KDA	X68102	Mycobacteri
38	26	3.2	1839	6	A28087	A28087	M.paratuber
39	26	3.2	1839	6	AR209771	AR209771	Sequence
40	26	3.2	3200	1	AF411607	AF411607	Mycobacte
41	26	3.2	303855	1	AE017230	AE017230	Mycobacte
42	24	3.0	24	6	AX513119	AX513119	Sequence
43	24	3.0	551	6	BD171694	BD171694	Identific
44	24	3.0	668	6	BD171691	BD171691	Identific
45	24	3.0	669	6	BD171690	BD171690	Identific

GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 14:16:30 ; Search time 561 Seconds
                                           (without alignments)
                                           8462.803 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg..........tggctgcgtacttcgccagc 802

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size :   19

Total number of hits satisfying chosen parameters: 117

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004as:*
                13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
  No.   Score Match Length DB ID   Description
----
      1   802 100.0   802 6 ABS70084   Abs70084 Mycobacte
      2   802 100.0   802 8 ABX10110   Abx10110 M. tuberc
      3   802 100.0 110000 4 AAI99682_10   Continuation (11 o
      4   751   93.6 110000 4 AAI99683_10   Continuation (11 o
      5   648   80.8   648 8 ABX10126   Abx10126 M. tuberc

6	579	72.2	648	8	ABX10127	Abx10127 M. bovis
7	577	71.9	628	6	ABS70085	Abs70085 Mycobacte
8	577	71.9	628	8	ABX10111	Abx10111 M. bovis
9	196	24.4	1058	2	AAT91444	Aat91444 Mycobacte
10	196	24.4	1058	2	AAT91508	Aat91508 Mycobacte
11	196	24.4	1058	2	AAV44383	Aav44383 Mycobacte
12	196	24.4	1058	2	AAV64491	Aav64491 M. tuberc
13	196	24.4	1058	2	AAZ19081	Aaz19081 M. tuberc
14	196	24.4	1058	2	AAZ19293	Aaz19293 M. tuberc
15	46	5.7	712	6	ABS70083	Abs70083 Mycobacte
16	46	5.7	712	8	ABX10109	Abx10109 M. szulga
17	31	3.9	570	8	ABX10133	Abx10133 M. szulga
18	31	3.9	588	8	ABX10132	Abx10132 M. gordon
19	31	3.9	745	6	ABS70079	Abs70079 Mycobacte
20	31	3.9	745	8	ABX10107	Abx10107 M. malmoe
21	31	3.9	881	8	ABX10113	Abx10113 M. avium
22	30	3.7	662	8	ABX10130	Abx10130 M. gastri
23	30	3.7	785	6	ABS70080	Abs70080 Mycobacte
24	30	3.7	785	8	ABX10104	Abx10104 M. gordon
25	29	3.6	631	8	ABX10131	Abx10131 M. kansas
26	29	3.6	642	6	ABS70078	Abs70078 Mycobacte
27	29	3.6	642	8	ABX10106	Abx10106 M. kansas
28	29	3.6	705	8	ABX10129	Abx10129 M. ulcera
29	29	3.6	706	8	ABX10128	Abx10128 M. marinu
30	28	3.5	768	8	ABX10125	Abx10125 M. simae
31	26	3.2	691	6	ABS70081	Abs70081 Mycobacte
32	26	3.2	698	6	ABS70082	Abs70082 Mycobacte
33	26	3.2	707	6	ABS70087	Abs70087 Mycobacte
34	26	3.2	707	8	ABX10114	Abx10114 M. paratu
35	26	3.2	727	8	ABX10123	Abx10123 M. paratu
36	26	3.2	727	8	ABX10122	Abx10122 M. avium
37	26	3.2	741	8	ABX10105	Abx10105 M. intrac
38	26	3.2	748	8	ABX10108	Abx10108 M. simae
39	26	3.2	761	8	ABX10124	Abx10124 M. malmoe
40	26	3.2	881	6	ABS70077	Abs70077 Mycobacte
41	26	3.2	1839	2	AAQ29147	Aaq29147 DNA encod
42	24	3.0	24	6	ABS70067	Abs70067 Mycobacte
43	24	3.0	685	6	ABS70089	Abs70089 Mycobacte
44	24	3.0	685	8	ABX10116	Abx10116 M. ulcera
45	24	3.0	686	6	ABS70088	Abs70088 Mycobacte

GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 18:32:59 ; Search time 185 Seconds
                                           (without alignments)
                                           7093.481 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg..........tggctgcgtacttcgccagc 802

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size :   19

Total number of hits satisfying chosen parameters: 34

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB   ID   Description
----
      1   802 100.0 4411529 3   US-09-103-840A-1   Sequence 1, Appli
      2   751   93.6 4403765 3   US-09-103-840A-2   Sequence 2, Appli
      3   196   24.4   1058 3   US-08-818-112-45   Sequence 45, Appl
      4   196   24.4   1058 3   US-08-818-111-45   Sequence 45, Appl
      5   196   24.4   1058 3   US-09-056-556-45   Sequence 45, Appl
      6   196   24.4   1058 3   US-09-072-596-45   Sequence 45, Appl
      7   196   24.4   1058 4   US-09-072-967-45   Sequence 45, Appl
      8   26   3.2   1839 3   US-08-122-458D-10   Sequence 10, Appl
      9   20   2.5   1983 4   US-09-902-540-3373   Sequence 3373, Ap
c   10   20   2.5   17125 4   US-09-902-540-1158   Sequence 1158, Ap
     11   19   2.4   717 3   US-09-124-238A-7   Sequence 7, Appli
     12   19   2.4   717 3   US-09-721-975-7   Sequence 7, Appli

	13	19	2.4	717	4	US-09-986-621-7	Sequence 7, Appli
	14	19	2.4	765	3	US-09-124-238A-21	Sequence 21, Appl
	15	19	2.4	765	3	US-09-721-975-21	Sequence 21, Appl
	16	19	2.4	765	4	US-09-986-621-21	Sequence 21, Appl
	17	19	2.4	1488	3	US-09-124-238A-8	Sequence 8, Appli
	18	19	2.4	1488	3	US-09-721-975-8	Sequence 8, Appli
	19	19	2.4	1488	4	US-09-986-621-8	Sequence 8, Appli
c	20	19	2.4	1589	4	US-09-634-238-68	Sequence 68, Appl
	21	19	2.4	1620	3	US-09-124-238A-32	Sequence 32, Appl
	22	19	2.4	1620	3	US-09-721-975-32	Sequence 32, Appl
	23	19	2.4	1620	4	US-09-986-621-32	Sequence 32, Appl
	24	19	2.4	1644	3	US-09-124-238A-9	Sequence 9, Appli
	25	19	2.4	1644	3	US-09-721-975-9	Sequence 9, Appli
	26	19	2.4	1644	4	US-09-986-621-9	Sequence 9, Appli
	27	19	2.4	1665	3	US-09-124-238A-33	Sequence 33, Appl
	28	19	2.4	1665	3	US-09-721-975-33	Sequence 33, Appl
	29	19	2.4	1665	4	US-09-986-621-33	Sequence 33, Appl
	30	19	2.4	1689	3	US-09-124-238A-22	Sequence 22, Appl
	31	19	2.4	1689	3	US-09-721-975-22	Sequence 22, Appl
	32	19	2.4	1689	4	US-09-986-621-22	Sequence 22, Appl
	33	19	2.4	1690	4	US-09-949-016-3384	Sequence 3384, Ap
	34	19	2.4	18196	4	US-09-949-016-15126	Sequence 15126, A

Run on: July 12, 2005, 19:19:37 ; Search time 643 Seconds
                                         (without alignments)
                                         7830.819 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg..........tggctgcgtacttcgccagc 802

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 6330945 seqs, 3139162390 residues

Word size :   19

Total number of hits satisfying chosen parameters: 82

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_NA:*
            1:   /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
            2:   /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
            3:   /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
            4:   /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
            5:   /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
            6:   /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
            7:   /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
            8:   /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
            9:   /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
           10:   /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
           11:   /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
           12:   /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
           13:   /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
           14:   /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
           15:   /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
           16:   /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
           17:   /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
           18:   /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
           19:   /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
           20:   /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
           21:   /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
           22:   /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
           23:   /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
           24:   /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
           25:   /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
           26:   /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query

	No.	Score	Match	Length	DB	ID	Description
	1	802	100.0	802	14	US-10-074-246-65	Sequence 65, Appl
	2	577	71.9	628	14	US-10-074-246-66	Sequence 66, Appl
	3	196	24.4	1058	15	US-10-193-002-45	Sequence 45, Appl
	4	196	24.4	1058	15	US-10-084-843-45	Sequence 45, Appl
	5	196	24.4	1058	24	US-11-028-898-45	Sequence 45, Appl
	6	46	5.7	712	14	US-10-074-246-64	Sequence 64, Appl
	7	31	3.9	745	14	US-10-074-246-60	Sequence 60, Appl
	8	30	3.7	785	14	US-10-074-246-61	Sequence 61, Appl
	9	29	3.6	642	14	US-10-074-246-59	Sequence 59, Appl
	10	26	3.2	691	14	US-10-074-246-62	Sequence 62, Appl
	11	26	3.2	698	14	US-10-074-246-63	Sequence 63, Appl
	12	26	3.2	707	14	US-10-074-246-68	Sequence 68, Appl
	13	26	3.2	881	14	US-10-074-246-58	Sequence 58, Appl
	14	24	3.0	24	14	US-10-074-246-48	Sequence 48, Appl
	15	24	3.0	685	14	US-10-074-246-70	Sequence 70, Appl
	16	24	3.0	686	14	US-10-074-246-69	Sequence 69, Appl
	17	22	2.7	22	9	US-09-817-014-72	Sequence 72, Appl
	18	22	2.7	22	14	US-10-074-246-25	Sequence 25, Appl
	19	22	2.7	22	16	US-10-056-229-72	Sequence 72, Appl
	20	22	2.7	219	14	US-10-074-246-73	Sequence 73, Appl
C	21	20	2.5	20	14	US-10-074-246-1	Sequence 1, Appli
	22	20	2.5	816	17	US-10-369-493-35898	Sequence 35898, A
	23	20	2.5	1491	18	US-10-425-114-22932	Sequence 22932, A
	24	20	2.5	1491	20	US-10-425-115-76519	Sequence 76519, A
	25	19	2.4	19	14	US-10-074-246-52	Sequence 52, Appl
	26	19	2.4	116	14	US-10-074-246-74	Sequence 74, Appl
C	27	19	2.4	334	20	US-10-425-115-23733	Sequence 23733, A
	28	19	2.4	705	20	US-10-425-115-76518	Sequence 76518, A
	29	19	2.4	717	9	US-09-986-621-7	Sequence 7, Appli
	30	19	2.4	717	10	US-09-986-625-7	Sequence 7, Appli
	31	19	2.4	717	16	US-10-292-951-7	Sequence 7, Appli
	32	19	2.4	717	17	US-10-382-844-7	Sequence 7, Appli
	33	19	2.4	765	9	US-09-986-621-21	Sequence 21, Appl
	34	19	2.4	765	10	US-09-986-625-21	Sequence 21, Appl
	35	19	2.4	765	16	US-10-292-951-21	Sequence 21, Appl
	36	19	2.4	765	17	US-10-382-844-21	Sequence 21, Appl
	37	19	2.4	886	20	US-10-425-115-9429	Sequence 9429, Ap
	38	19	2.4	1456	16	US-10-292-951-37	Sequence 37, Appl
	39	19	2.4	1456	17	US-10-382-844-37	Sequence 37, Appl
C	40	19	2.4	1456	19	US-10-437-963-82805	Sequence 82805, A
C	41	19	2.4	1478	20	US-10-363-345A-16713	Sequence 16713, A
	42	19	2.4	1478	20	US-10-363-345A-16714	Sequence 16714, A
C	43	19	2.4	1478	21	US-10-363-483A-16713	Sequence 16713, A
	44	19	2.4	1478	21	US-10-363-483A-16714	Sequence 16714, A
	45	19	2.4	1488	9	US-09-986-621-8	Sequence 8, Appli

Search completed: July 12, 2005, 21:34:28
Job time : 644 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 18:22:18 ; Search time 3388 Seconds
                                           (without alignments)
                                           9010.491 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg..........tggctgcgtacttcgccagc 802

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size :   19

Total number of hits satisfying chosen parameters: 163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
    No.   Score   Match Length DB   ID   Description

 C   1   20   2.5   339   5   BP087522   BP087522 BP087522
 C   2   20   2.5   439   6   CD036612   CD036612 mgsu010xL
     3   20   2.5   642   5   BP125333   BP125333 BP125333
     4   20   2.5   693   8   BZ654250   BZ654250 OGANC18TC
 C   5   20   2.5   709   9   CG101385   CG101385 PUIDS38TD
 C   6   20   2.5   788   9   CG368128   CG368128 OGYBX73TH

	7	20	2.5	790	9	CG101383	CG101383	PUIDS38TB
c	8	20	2.5	794	4	BM415165	BM415165	OP20237 M
	9	20	2.5	807	8	CC360524	CC360524	PUHHB49TD
c	10	20	2.5	811	8	BZ640143	BZ640143	OGAOY76TC
	11	20	2.5	820	9	CC717618	CC717618	OGOAK51TH
c	12	20	2.5	836	2	BE641565	BE641565	Cri2_3_K0
c	13	20	2.5	836	9	CG355150	CG355150	OG0FI18TV
	14	20	2.5	841	9	CG128824	CG128824	PUFSB83TB
	15	20	2.5	843	9	CG350861	CG350861	OGXFO45TH
c	16	20	2.5	858	9	CG334280	CG334280	OG0FN56TH
	17	20	2.5	859	9	CG297677	CG297677	OG3DH69TH
c	18	20	2.5	866	9	CG310598	CG310598	OGWGW48TH
	19	20	2.5	881	9	CG310605	CG310605	OGWGW48TV
	20	20	2.5	881	9	CG368142	CG368142	OGYBX73TV
c	21	20	2.5	884	9	CC717628	CC717628	OGOAK51TV
	22	20	2.5	923	9	CG334290	CG334290	OG0FN56TV
	23	20	2.5	925	9	CG363674	CG363674	OG1CR45TV
c	24	20	2.5	933	9	CG456197	CG456197	PUIJX77TD
	25	20	2.5	1025	9	CG456153	CG456153	PUIJX77TB
c	26	20	2.5	1487	2	BF698864	BF698864	602126433
	27	20	2.5	1513	9	AG152149	AG152149	Pan trogl
c	28	19	2.4	139	8	CC380210	CC380210	PUHGX06TD
c	29	19	2.4	148	9	CL303432	CL303432	M051C08 G
c	30	19	2.4	309	5	BW575850	BW575850	BW575850
	31	19	2.4	332	1	AV903172	AV903172	AV903172
	32	19	2.4	335	4	BM848612	BM848612	K-EST0128
c	33	19	2.4	343	6	CB655053	CB655053	OSJNEc08B
	34	19	2.4	356	1	AA280978	AA280978	zs97f03.r
c	35	19	2.4	372	1	AB009130	AB009130	AB009130
	36	19	2.4	404	5	BY032959	BY032959	BY032959
	37	19	2.4	433	5	BW509786	BW509786	BW509786
	38	19	2.4	511	2	BE302649	BE302649	ba73f02.y
	39	19	2.4	520	1	AV864667	AV864667	AV864667
	40	19	2.4	523	9	CG617736	CG617736	OST311668
	41	19	2.4	531	9	CG653478	CG653478	OST418882
	42	19	2.4	544	9	CG662435	CG662435	OST445990
	43	19	2.4	560	9	CG645739	CG645739	OST390727
	44	19	2.4	580	5	BP302387	BP302387	BP302387
	45	19	2.4	583	5	BP235848	BP235848	BP235848

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 5482.32 Seconds
                                           (without alignments)
                                           7088.436 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg..........tggctgcgtacttcgccagc 802

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
      1   802   100.0   802   6   AX513136   AX513136 Sequence
      2   802   100.0 327650   1   BX248337   BX248337 Mycobacte
      3   802   100.0 349306   1   BX842575   BX842575 Mycobacte

4	801.6	100.0	110000	1	AE000516_10	Continuation (11 o
5	626.4	78.1	628	6	AX513137	AX513137 Sequence
6	449.2	56.0	611	6	BD171688	BD171688 Identific
7	447.6	55.8	611	6	BD171689	BD171689 Identific
8	416.6	51.9	712	6	AX513135	AX513135 Sequence
9	408.6	50.9	785	6	AX513132	AX513132 Sequence
10	407.6	50.8	881	6	AX513129	AX513129 Sequence
11	407.6	50.8	1832	1	MP34KDA	X68102 Mycobacteri
12	407.6	50.8	1839	6	A28087	A28087 M.paratuber
13	407.6	50.8	3200	1	AF411607	AF411607 Mycobacte
14	407.6	50.8	303855	1	AE017230	AE017230 Mycobacte
15	406	50.6	1839	6	AR209771	AR209771 Sequence
16	384.6	48.0	685	6	AX513141	AX513141 Sequence
17	383.8	47.9	691	6	AX513133	AX513133 Sequence
18	375.2	46.8	686	6	AX513140	AX513140 Sequence
19	370.8	46.2	707	6	AX513139	AX513139 Sequence
20	369	46.0	369	6	BD171700	BD171700 Identific
21	354.8	44.2	698	6	AX513134	AX513134 Sequence
22	351.4	43.8	745	6	AX513131	AX513131 Sequence
23	321.4	40.1	323	6	BD171699	BD171699 Identific
24	320.2	39.9	642	6	AX513130	AX513130 Sequence
25	269.2	33.6	110000	1	AP006618_27	Continuation (28 o
26	266.6	33.2	37304	1	MLCL373	AL035500 Mycobacte
27	266.6	33.2	344050	1	MLEPRTN1	AL583917 Mycobacte
28	239	29.8	668	6	BD171691	BD171691 Identific
29	238	29.7	729	6	AX513142	AX513142 Sequence
30	229.6	28.6	669	6	BD171690	BD171690 Identific
31	229.4	28.6	724	6	BD171686	BD171686 Identific
32	220	27.4	690	6	BD171684	BD171684 Identific
33	220	27.4	690	6	BD171685	BD171685 Identific
34	216.4	27.0	1058	6	AR169193	AR169193 Sequence
35	216.4	27.0	1058	6	BD205858	BD205858 Compounds
36	216.4	27.0	1058	6	CQ785444	CQ785444 Sequence
37	216.4	27.0	1058	6	AR182483	AR182483 Sequence
38	216.4	27.0	1058	6	AR194866	AR194866 Sequence
39	216.4	27.0	1058	6	AR233138	AR233138 Sequence
40	216.4	27.0	1058	6	AR353343	AR353343 Sequence
41	216.4	27.0	1058	6	AX429637	AX429637 Sequence
42	216.4	27.0	1058	6	AX832622	AX832622 Sequence
43	216.4	27.0	1058	6	BD006366	BD006366 Compounds
44	216.4	27.0	1058	6	BD006486	BD006486 Compounds
45	216.4	27.0	1058	6	BD069326	BD069326 Compounds

GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 960.512 Seconds
                                            (without alignments)
                                            4942.816 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg..........tggctgcgtacttcgccagc 802

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                  1: geneseqn1980s:*
                  2: geneseqn1990s:*
                  3: geneseqn2000s:*
                  4: geneseqn2001as:*
                  5: geneseqn2001bs:*
                  6: geneseqn2002as:*
                  7: geneseqn2002bs:*
                  8: geneseqn2003as:*
                  9: geneseqn2003bs:*
                  10: geneseqn2003cs:*
                  11: geneseqn2003ds:*
                  12: geneseqn2004as:*
                  13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
       1   802   100.0   802 6   ABS70084   Abs70084 Mycobacte
       2   802   100.0   802 8   ABX10110   Abx10110 M. tuberc
       3   802   100.0 110000 4   AAI99682_10   Continuation (11 o
       4   801.6   100.0 110000 4   AAI99683_10   Continuation (11 o
       5   648   80.8   648 8   ABX10126   Abx10126 M. tuberc

6	643.2	80.2	648	8	ABX10127	Abx10127	M. bovis
7	626.4	78.1	628	6	ABS70085	Abs70085	Mycobacte
8	626.4	78.1	628	8	ABX10111	Abx10111	M. bovis
9	416.6	51.9	712	6	ABS70083	Abs70083	Mycobacte
10	416.6	51.9	712	8	ABX10109	Abx10109	M. szulga
11	410.8	51.2	881	8	ABX10113	Abx10113	M. avium
12	408.6	50.9	785	6	ABS70080	Abs70080	Mycobacte
13	408.6	50.9	785	8	ABX10104	Abx10104	M. gordon
14	407.6	50.8	881	6	ABS70077	Abs70077	Mycobacte
15	407.6	50.8	1839	2	AAQ29147	Aaq29147	DNA encod
16	384.6	48.0	685	6	ABS70089	Abs70089	Mycobacte
17	384.6	48.0	685	8	ABX10116	Abx10116	M. ulcera
18	384.6	48.0	705	8	ABX10129	Abx10129	M. ulcera
19	383.8	47.9	691	6	ABS70081	Abs70081	Mycobacte
20	383.8	47.9	741	8	ABX10105	Abx10105	M. intrac
21	383.8	47.9	761	8	ABX10124	Abx10124	M. malmoe
22	380	47.4	706	8	ABX10128	Abx10128	M. marinu
23	375.2	46.8	686	6	ABS70088	Abs70088	Mycobacte
24	375.2	46.8	686	8	ABX10115	Abx10115	M. marinu
25	370.8	46.2	707	6	ABS70087	Abs70087	Mycobacte
26	370.8	46.2	727	8	ABX10123	Abx10123	M. paratu
27	370.8	46.2	727	8	ABX10122	Abx10122	M. avium
28	369.2	46.0	707	8	ABX10114	Abx10114	M. paratu
29	359	44.8	570	8	ABX10133	Abx10133	M. szulga
30	358	44.6	768	8	ABX10125	Abx10125	M. simae
31	354.8	44.2	698	6	ABS70082	Abs70082	Mycobacte
32	354.8	44.2	748	8	ABX10108	Abx10108	M. simae
33	351.4	43.8	745	6	ABS70079	Abs70079	Mycobacte
34	351.4	43.8	745	8	ABX10107	Abx10107	M. malmoe
35	326.8	40.7	631	8	ABX10131	Abx10131	M. kansas
36	325	40.5	662	8	ABX10130	Abx10130	M. gastri
37	320.2	39.9	642	6	ABS70078	Abs70078	Mycobacte
38	320.2	39.9	642	8	ABX10106	Abx10106	M. kansas
39	292	36.4	588	8	ABX10132	Abx10132	M. gordon
40	238	29.7	729	6	ABS70090	Abs70090	Mycobacte
41	238	29.7	729	8	ABX10117	Abx10117	M. leprae
42	236.2	29.5	727	8	ABX10134	Abx10134	M. leprae
43	216.4	27.0	1058	2	AAT91444	Aat91444	Mycobacte
44	216.4	27.0	1058	2	AAT91508	Aat91508	Mycobacte
45	216.4	27.0	1058	2	AAV44383	Aav44383	Mycobacte

GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:18:20 ; Search time 283.234 Seconds
                                              (without alignments)
                                            4633.247 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg..........tggctgcgtacttcgccagc 802

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
     No.   Score   Match Length DB   ID   Description
    ----
         1   802   100.0 4411529 3   US-09-103-840A-1   · Sequence 1, Appli
         2   801.6   100.0 4403765 3   US-09-103-840A-2   Sequence 2, Appli
         3   406   50.6   1839 3   US-08-122-458D-10   Sequence 10, Appl
         4   216.4   27.0   1058 3   US-08-818-112-45   Sequence 45, Appl
         5   216.4   27.0   1058 3   US-08-818-111-45   Sequence 45, Appl
         6   216.4   27.0   1058 3   US-09-056-556-45   Sequence 45, Appl
         7   216.4   27.0   1058 3   US-09-072-596-45   Sequence 45, Appl
         8   216.4   27.0   1058 4   US-09-072-967-45   Sequence 45, Appl
         9   89.2   11.1   597 3   US-08-122-458D-17   Sequence 17, Appl
  c   10   71.6   8.9   1185 4   US-09-894-844-71   Sequence 71, Appl
  c   11   71.6   8.9 4403765 3   US-09-103-840A-2   Sequence 2, Appli
  c   12   71.6   8.9 4411529 3   US-09-103-840A-1   Sequence 1, Appli

C	13	70.4	8.8	888	3	US-09-655-270A-6	Sequence 6, Appli
C	14	70.4	8.8	888	3	US-09-651-941-6	Sequence 6, Appli
C	15	70.4	8.8	888	3	US-09-955-597-6	Sequence 6, Appli
C	16	70.4	8.8	12508	3	US-09-655-270A-1	Sequence 1, Appli
C	17	70.4	8.8	12523	3	US-09-651-941-1	Sequence 1, Appli
C	18	70.4	8.8	12523	3	US-09-955-597-1	Sequence 1, Appli
C	19	61	7.6	825	4	US-09-266-965-58	Sequence 58, Appl
	20	61	7.6	53500	4	US-09-266-965-76	Sequence 76, Appl
	21	50.2	6.3	402	4	US-09-252-991A-15772	Sequence 15772, A
C	22	50.2	6.3	999	4	US-09-252-991A-15890	Sequence 15890, A
C	23	50.2	6.3	1086	4	US-09-252-991A-15921	Sequence 15921, A
	24	50.2	6.3	1284	4	US-09-252-991A-15802	Sequence 15802, A
C	25	50.2	6.3	3390	4	US-09-902-540-6647	Sequence 6647, Ap
	26	50.2	6.3	3393	4	US-09-902-540-514	Sequence 514, App
C	27	48.8	6.1	1185	4	US-09-252-991A-3103	Sequence 3103, Ap
C	28	48.8	6.1	2592	4	US-09-252-991A-3003	Sequence 3003, Ap
C	29	46	5.7	1149	4	US-09-266-965-41	Sequence 41, Appl
C	30	45	5.6	4284	4	US-09-902-540-3289	Sequence 3289, Ap
	31	45	5.6	17727	4	US-09-902-540-1152	Sequence 1152, Ap
	32	44.4	5.5	450	4	US-09-252-991A-664	Sequence 664, App
	33	44.4	5.5	1728	4	US-09-252-991A-616	Sequence 616, App
C	34	42.6	5.3	1155	4	US-09-902-540-4958	Sequence 4958, Ap
C	35	42.6	5.3	1170	4	US-09-252-991A-5515	Sequence 5515, Ap
	36	42.6	5.3	1434	4	US-09-252-991A-5626	Sequence 5626, Ap
C	37	42.6	5.3	1992	4	US-09-252-991A-5567	Sequence 5567, Ap
C	38	42.6	5.3	6975	4	US-09-902-540-2386	Sequence 2386, Ap
	39	42.6	5.3	17315	4	US-09-902-540-1103	Sequence 1103, Ap
C	40	42.6	5.3	27219	4	US-09-902-540-1244	Sequence 1244, Ap
C	41	42.4	5.3	30001	1	US-08-125-468-1	Sequence 1, Appli
C	42	42.4	5.3	30001	2	US-08-474-933-1	Sequence 1, Appli
C	43	42.2	5.3	47981	4	US-09-679-279-1	Sequence 1, Appli
C	44	42	5.2	1695	4	US-09-902-540-8849	Sequence 8849, Ap
C	45	42	5.2	9993	4	US-09-902-540-942	Sequence 942, App

GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 11:13:07 ; Search time 1166.73 Seconds
                                              (without alignments)
                                            4315.680 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg..........tggctgcgtacttcgccagc 802

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 6330945 seqs, 3139162390 residues

Total number of hits satisfying chosen parameters: 12661890

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                  1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                  2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                  3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                  4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                  5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                  6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                  7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                  8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                  9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                  10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                  11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                  12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                  13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                  14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                  15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                  16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                  17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                  18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                  19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                  20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
                  21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
                  22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                  23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                  24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                  25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                  26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	802	100.0	802	14	US-10-074-246-65	Sequence 65, Appl
	2	626.4	78.1	628	14	US-10-074-246-66	Sequence 66, Appl
	3	416.6	51.9	712	14	US-10-074-246-64	Sequence 64, Appl
	4	408.6	50.9	785	14	US-10-074-246-61	Sequence 61, Appl
	5	407.6	50.8	881	14	US-10-074-246-58	Sequence 58, Appl
	6	384.6	48.0	685	14	US-10-074-246-70	Sequence 70, Appl
	7	383.8	47.9	691	14	US-10-074-246-62	Sequence 62, Appl
	8	375.2	46.8	686	14	US-10-074-246-69	Sequence 69, Appl
	9	370.8	46.2	707	14	US-10-074-246-68	Sequence 68, Appl
	10	354.8	44.2	698	14	US-10-074-246-63	Sequence 63, Appl
	11	351.4	43.8	745	14	US-10-074-246-60	Sequence 60, Appl
	12	320.2	39.9	642	14	US-10-074-246-59	Sequence 59, Appl
	13	238	29.7	729	14	US-10-074-246-71	Sequence 71, Appl
	14	216.4	27.0	1058	15	US-10-193-002-45	Sequence 45, Appl
	15	216.4	27.0	1058	15	US-10-084-843-45	Sequence 45, Appl
	16	216.4	27.0	1058	24	US-11-028-898-45	Sequence 45, Appl
	17	122.6	15.3	9025608	15	US-10-156-761-1	Sequence 1, Appli
C	18	121.8	15.2	825	15	US-10-156-761-7462	Sequence 7462, Ap
	19	117.2	14.6	400	14	US-10-074-246-67	Sequence 67, Appl
C	20	71.6	8.9	1185	9	US-09-894-844-71	Sequence 71, Appl
C	21	71.6	8.9	1185	17	US-10-388-902-71	Sequence 71, Appl
C	22	71.6	8.9	1185	18	US-10-647-089-71	Sequence 71, Appl
C	23	71.6	8.9	1188	17	US-10-282-122A-28727	Sequence 28727, A
C	24	70.4	8.8	888	9	US-09-955-597-6	Sequence 6, Appli
C	25	70.4	8.8	12523	9	US-09-955-597-1	Sequence 1, Appli
C	26	63.2	7.9	9521	18	US-10-168-663-18	Sequence 18, Appl
	27	63.2	7.9	9521	18	US-10-168-663-19	Sequence 19, Appl
C	28	61.8	7.7	816	15	US-10-156-761-581	Sequence 581, App
C	29	61.8	7.7	927	15	US-10-156-761-3786	Sequence 3786, Ap
C	30	61.8	7.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
C	31	61	7.6	825	10	US-09-953-348-58	Sequence 58, Appl
C	32	61	7.6	825	15	US-10-267-255-58	Sequence 58, Appl
	33	61	7.6	53500	10	US-09-953-348-76	Sequence 76, Appl
	34	61	7.6	53500	15	US-10-267-255-76	Sequence 76, Appl
C	35	57	7.1	927	15	US-10-156-761-6872	Sequence 6872, Ap
C	36	54.2	6.8	978	15	US-10-156-761-2643	Sequence 2643, Ap
C	37	50.2	6.3	1002	9	US-09-815-242-7774	Sequence 7774, Ap
C	38	47.8	6.0	1014	15	US-10-156-761-6996	Sequence 6996, Ap
C	39	47.8	6.0	1287	15	US-10-156-761-832	Sequence 832, App
C	40	46	5.7	1149	10	US-09-953-348-41	Sequence 41, Appl
C	41	46	5.7	1149	15	US-10-267-255-41	Sequence 41, Appl
	42	45.8	5.7	1371	17	US-10-282-122A-15021	Sequence 15021, A
	43	45.6	5.7	1818	17	US-10-282-122A-14315	Sequence 14315, A
C	44	45.4	5.7	1704	17	US-10-282-122A-13510	Sequence 13510, A
	45	45.4	5.7	1752	17	US-10-282-122A-13696	Sequence 13696, A

GenCore version 5.1.6
                  Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:06:45 ; Search time 6338.48 Seconds
                                             (without alignments)
                                             4816.222 Million cell updates/sec

Title: US-10-074-246-65
Perfect score: 802
Sequence: 1 tcatagcaggcctcctcttg..........tggctgcgtacttcgccagc 802

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   . EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                                  SUMMARIES
                         %
Result   Query
     No.   Score   Match Length DB   ID   Description
     ----
     c   1   58.2   7.3   925   9   CNS0091P   AL053013 Drosophil
         2   56.4   7.0   925   9   CNS0091P   AL053013 Drosophil
     c   3   56.4   7.0   935   9   CNS006XK   AL066051 Drosophil
     c   4   51.4   6.4   985   6   CA981964   CA981964 AGENCOURT
     c   5   50.6   6.3   645   9   CNS012I3   AL101589 Drosophil
     c   6   50.2   6.3   1028   8   BZ550423   BZ550423 pacs1-60_
     c   7   50.2   6.3   1399   8   BZ554759   BZ554759 pacs1-60_
     c   8   48.8   6.1   1101   9   CNS017SY   AL108460 Drosophil
         9   47.8   6.0   645   9   CNS012I3   AL101589 Drosophil

	10	47.2	5.9	1752	9	CL972165	CL972165	OsIFCC041
	11	47	5.9	1339	4	BM458211	BM458211	AGENCOURT
c	12	46.8	5.8	932	9	CNS0072Q	AL066742	Drosophil
	13	46.6	5.8	1038	7	CK206930	CK206930	FGAS01854
	14	46.2	5.8	832	9	AG108460	AG108460	Pan trogl
c	15	46	5.7	1462	9	AG441877	AG441877	Mus muscu
	16	45.8	5.7	802	8	BZ675208	BZ675208	PUBAL48TD
	17	45.8	5.7	1452	9	AG032979	AG032979	Pan trogl
c	18	45.4	5.7	650	8	CC331276	CC331276	OGUAF63TH
c	19	45.4	5.7	711	7	CO520370	CO520370	3530_1_13
	20	45.4	5.7	725	6	CD423375	CD423375	SA1_28_D1
	21	45.4	5.7	1328	9	AG043615	AG043615	Pan trogl
c	22	45.2	5.6	767	8	AQ847229	AQ847229	LMAJFV1_1
c	23	45.2	5.6	851	6	CB908312	CB908312	tric084xp
	24	44.6	5.6	932	9	CNS0072Q	AL066742	Drosophil
c	25	44.6	5.6	961	5	BQ673489	BQ673489	AGENCOURT
	26	44.4	5.5	1021	8	BZ559395	BZ559395	pacs2-164
c	27	44.4	5.5	1045	8	BZ564504	BZ564504	pacs2-164
c	28	44.4	5.5	1119	8	BZ560644	BZ560644	pacs2-164
	29	44.4	5.5	1516	4	BG809984	BG809984	mgct002xd
	30	44.2	5.5	776	9	CG218187	CG218187	OGYAP34TV
	31	44.2	5.5	935	9	CNS006XK	AL066051	Drosophil
c	32	44	5.5	513	8	BZ896393	BZ896393	NaRP9_014
	33	44	5.5	1598	9	AG030579	AG030579	Pan trogl
	34	43.8	5.5	553	2	BF277572	BF277572	GA__Eb003
c	35	43.8	5.5	794	8	BZ564793	BZ564793	pacs2-164
	36	43.6	5.4	317	4	BI417136	BI417136	949053F04
	37	43.6	5.4	317	4	BI674168	BI674168	949053F04
	38	43.6	5.4	549	4	BI358830	BI358830	949041E06
	39	43.6	5.4	606	4	BI595873	BI595873	949073A06
	40	43.4	5.4	430	6	CB644339	CB644339	OSJNEb05I
c	41	43.4	5.4	618	7	CF303450	CF303450	ABF1--02-
	42	43.4	5.4	676	6	CB649863	CB649863	OSJNEb14A
	43	43.4	5.4	692	6	CB654140	CB654140	OSJNEc05N
	44	43.4	5.4	697	6	CB656121	CB656121	OSJNEc10B

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 4832.92 Seconds
                                            (without alignments)
                                            7088.436 Million cell updates/sec

Title: US-10-074-246-68
Perfect score: 707
Sequence: 1 tcgtagctggcttcctcgtc..........aaaaggcagtggaagcaaca 707

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                  1: gb_ba:*
                  2: gb_htg:*
                  3: gb_in:*
                  4: gb_om:*
                  5: gb_ov:*
                  6: gb_pat:*
                  7: gb_ph:*
                  8: gb_pl:*
                  9: gb_pr:*
                  10: gb_ro:*
                  11: gb_sts:*
                  12: gb_sy:*
                  13: gb_un:*
                  14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                         %
Result   Query
    No.   Score   Match   Length   DB   ID   Description
    ----
       1   707   100.0   707   6   AX513139   AX513139 Sequence
       2   707   100.0   1832   1   MP34KDA   X68102 Mycobacteri
       3   707   100.0   1839   6   A28087   A28087 M.paratuber

4	707	100.0	3200	1	AF411607	AF411607 Mycobacte
5	707	100.0	303855	1	AE017230	AE017230 Mycobacte
6	705.4	99.8	881	6	AX513129	AX513129 Sequence
7	705.4	99.8	1839	6	AR209771	AR209771 Sequence
8	529	74.8	690	6	BD171685	BD171685 Identific
9	527.4	74.6	690	6	BD171684	BD171684 Identific
10	426.6	60.3	691	6	AX513133	AX513133 Sequence
11	422	59.7	448	6	BD171701	BD171701 Identific
12	411.8	58.2	698	6	AX513134	AX513134 Sequence
13	383.8	54.3	685	6	AX513141	AX513141 Sequence
14	376	53.2	686	6	AX513140	AX513140 Sequence
15	370.8	52.4	802	6	AX513136	AX513136 Sequence
16	370.8	52.4	110000	1	AE000516_10	Continuation (11 o
17	370.8	52.4	327650	1	BX248337	BX248337 Mycobacte
18	370.8	52.4	349306	1	BX842575	BX842575 Mycobacte
19	369.2	52.2	628	6	AX513137	AX513137 Sequence
20	350.6	49.6	785	6	AX513132	AX513132 Sequence
21	344.2	48.7	712	6	AX513135	AX513135 Sequence
22	330.2	46.7	642	6	AX513130	AX513130 Sequence
23	312.6	44.2	745	6	AX513131	AX513131 Sequence
24	283.8	40.1	110000	1	AP006618_27	Continuation (28 o
25	265	37.5	724	6	BD171686	BD171686 Identific
26	257.8	36.5	731	6	BD171687	BD171687 Identific
27	241.8	34.2	37304	1	MLCL373	AL035500 Mycobacte
28	241.8	34.2	344050	1	MLEPRTN1	AL583917 Mycobacte
29	236.4	33.4	729	6	AX513142	AX513142 Sequence
30	229.8	32.5	668	6	BD171691	BD171691 Identific
31	222	31.4	669	6	BD171690	BD171690 Identific
32	215.4	30.5	217	6	BD171702	BD171702 Identific
33	211.6	29.9	611	6	BD171688	BD171688 Identific
34	210	29.7	611	6	BD171689	BD171689 Identific
35	187.2	26.5	594	6	BD171693	BD171693 Identific
36	182.4	25.8	533	6	BD171695	BD171695 Identific
37	173.6	24.6	625	6	BD171692	BD171692 Identific
38	168.2	23.8	551	6	BD171694	BD171694 Identific
39	164.2	23.2	369	6	BD171700	BD171700 Identific
40	147.4	20.8	343	6	BD171697	BD171697 Identific
41	144.8	20.5	323	6	BD171699	BD171699 Identific
42	144.8	20.5	37586	6	AX191745	AX191745 Sequence
43	144.8	20.5	110000	1	AE000516_24	Continuation (25 o
44	144.8	20.5	306050	1	BX248341	BX248341 Mycobacte
45	144.8	20.5	346186	1	BX842578	BX842578 Mycobacte

GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 846.735 Seconds
                                             (without alignments)
                                             4942.816 Million cell updates/sec

Title: .   US-10-074-246-68
Perfect score: 707
Sequence: 1 tcgtagctggcttcctcgtc..........aaaaggcagtggaagcaaca 707

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                   1: geneseqn1980s:*
                   2: geneseqn1990s:*
                   3: geneseqn2000s:*
                   4: geneseqn2001as:*
                   5: geneseqn2001bs:*
                   6: geneseqn2002as:*
                   7: geneseqn2002bs:*
                   8: geneseqn2003as:*
                   9: geneseqn2003bs:*
                   10: geneseqn2003cs:*
                   11: geneseqn2003ds:*
                   12: geneseqn2004as:*
                   13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                         %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
      1   707   100.0   707 6   ABS70087   Abs70087 Mycobacte
      2   707   100.0   727 8   ABX10123   Abx10123 M. paratu
      3   707   100.0   1839 2   AAQ29147   Aaq29147 DNA encod
      4   705.4   99.8   707 8   ABX10114   Abx10114 M. paratu
      5   705.4   99.8   727 8   ABX10122   Abx10122 M. avium

6	705.4	99.8	881	6	ABS70077	Abs70077 Mycobacte
7	702.2	99.3	881	8	ABX10113	Abx10113 M. avium
8	433.4	61.3	761	8	ABX10124	Abx10124 M. malmoe
9	430.2	60.8	741	8	ABX10105	Abx10105 M. intrac
10	426.6	60.3	691	6	ABS70081	Abs70081 Mycobacte
11	415	58.7	768	8	ABX10125	Abx10125 M. simae
12	411.8	58.2	698	6	ABS70082	Abs70082 Mycobacte
13	411.8	58.2	748	8	ABX10108	Abx10108 M. simae
14	391.8	55.4	705	8	ABX10129	Abx10129 M. ulcera
15	383.8	54.3	685	6	ABS70089	Abs70089 Mycobacte
16	383.8	54.3	685	8	ABX10116	Abx10116 M. ulcera
17	380.8	53.9	706	8	ABX10128	Abx10128 M. marinu
18	376	53.2	686	6	ABS70088	Abs70088 Mycobacte
19	376	53.2	686	8	ABX10115	Abx10115 M. marinu
20	370.8	52.4	648	8	ABX10126	Abx10126 M. tuberc
21	370.8	52.4	648	8	ABX10127	Abx10127 M. bovis
22	370.8	52.4	802	6	ABS70084	Abs70084 Mycobacte
23	370.8	52.4	802	8	ABX10110	Abx10110 M. tuberc
24	370.8	52.4	110000	4	AAI99682_10	Continuation (11 o
25	370.8	52.4	110000	4	AAI99683_10	Continuation (11 o
26	369.2	52.2	628	6	ABS70085	Abs70085 Mycobacte
27	369.2	52.2	628	8	ABX10111	Abx10111 M. bovis
28	352.2	49.8	570	8	ABX10133	Abx10133 M. szulga
29	350.6	49.6	631	8	ABX10131	Abx10131 M. kansas
30	350.6	49.6	785	6	ABS70080	Abs70080 Mycobacte
31	350.6	49.6	785	8	ABX10104	Abx10104 M. gordon
32	344.2	48.7	712	6	ABS70083	Abs70083 Mycobacte
33	344.2	48.7	712	8	ABX10109	Abx10109 M. szulga
34	330.2	46.7	642	6	ABS70078	Abs70078 Mycobacte
35	330.2	46.7	642	8	ABX10106	Abx10106 M. kansas
36	330.2	46.7	662	8	ABX10130	Abx10130 M. gastri
37	312.6	44.2	745	6	ABS70079	Abs70079 Mycobacte
38	312.6	44.2	745	8	ABX10107	Abx10107 M. malmoe
39	309.4	43.8	588	8	ABX10132	Abx10132 M. gordon
40	254.8	36.0	727	8	ABX10134	Abx10134 M. leprae
41	236.4	33.4	729	6	ABS70090	Abs70090 Mycobacte
42	236.4	33.4	729	8	ABX10117	Abx10117 M. leprae
43	150	21.2	373	8	ABX10135	Abx10135 M. intrac
44	144.8	20.5	110000	4	AAI99682_24	Continuation (25 o
45	144.8	20.5	110000	4	AAI99683_24	Continuation (25 o

Search completed: July 12, 2005, 14:48:36
Job time : 848.735 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:18:20 ; Search time 249.684 Seconds
                                          (without alignments)
                                          4633.247 Million cell updates/sec

Title: US-10-074-246-68
Perfect score: 707
Sequence: 1 tcgtagctggcttcctcgtc..........aaaaggcagtggaagcaaca 707

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
    No.   Score   Match Length DB   ID   Description
----
      1   705.4   99.8   1839 3   US-08-122-458D-10   Sequence 10, Appl
    · 2   370.8   52.4 4403765 3   US-09-103-840A-2   Sequence 2, Appli
      3   370.8   52.4 4411529 3   US-09-103-840A-1   Sequence 1, Appli
c   4   70.4   10.0   888 3   US-09-655-270A-6   Sequence 6, Appli
c   5   70.4   10.0   888 3   US-09-651-941-6   Sequence 6, Appli
c   6   70.4   10.0   888 3   US-09-955-597-6   Sequence 6, Appli
c   7   70.4   10.0   ·12508 3   US-09-655-270A-1   Sequence 1, Appli
c   8   70.4   10.0   12523 3   US-09-651-941-1   Sequence 1, Appli
c   9   70.4   10.0   12523 3   US-09-955-597-1   Sequence 1, Appli

C	10	65.4	9.3	1185	4	US-09-894-844-71	Sequence 71, Appl
C	11	65.4	9.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C	12	65.4	9.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C	13	64.4	9.1	825	4	US-09-266-965-58	Sequence 58, Appl
	14	64.4	9.1	53500	4	US-09-266-965-76	Sequence 76, Appl
C	15	62	8.8	795	4	US-09-266-965-57	Sequence 57, Appl
C	16	62	8.8	53500	4	US-09-266-965-76	Sequence 76, Appl
C	17	56.4	8.0	4089	4	US-09-902-540-7372	Sequence 7372, Ap
	18	56.4	8.0	4090	4	US-09-902-540-706	Sequence 706, App
C	19	54.8	7.8	1185	4	US-09-252-991A-3103	Sequence 3103, Ap
C	20	54.8	7.8	2592	4	US-09-252-991A-3003	Sequence 3003, Ap
C	21	52.8	7.5	328	3	US-09-060-756-406	Sequence 406, App
C	22	52.8	7.5	328	4	US-09-670-314-406	Sequence 406, App
C	23	52.2	7.4	355	3	US-09-060-756-390	Sequence 390, App
C	24	52.2	7.4	355	4	US-09-670-314-390	Sequence 390, App
C	25	52.2	7.4	438	3	US-09-060-756-112	Sequence 112, App
C	26	52.2	7.4	438	4	US-09-670-314-112	Sequence 112, App
C	27	51.8	7.3	308	3	US-09-060-756-532	Sequence 532, App
C	28	51.8	7.3	308	4	US-09-670-314-532	Sequence 532, App
	29	51.4	7.3	402	4	US-09-252-991A-15772	Sequence 15772, A
C	30	51.4	7.3	999	4	US-09-252-991A-15890	Sequence 15890, A
C	31	51.4	7.3	1086	4	US-09-252-991A-15921	Sequence 15921, A
	32	51.4	7.3	1284	4	US-09-252-991A-15802	Sequence 15802, A
C	33	51.2	7.2	6975	4	US-09-902-540-2386	Sequence 2386, Ap
	34	51.2	7.2	17315	4	US-09-902-540-1103	Sequence 1103, Ap
C	35	50.4	7.1	3390	4	US-09-902-540-6647	Sequence 6647, Ap
	36	50.4	7.1	3393	4	US-09-902-540-514	Sequence 514, App
C	37	49.2	7.0	30001	1	US-08-125-468-1	Sequence 1, Appli
C	38	49.2	7.0	30001	2	US-08-474-933-1	Sequence 1, Appli
C	39	48.2	6.8	303	3	US-09-060-756-468	Sequence 468, App
C	40	48.2	6.8	303	4	US-09-670-314-468	Sequence 468, App
C	41	48.2	6.8	2427	4	US-09-902-540-5377	Sequence 5377, Ap
C	42	48.2	6.8	34552	4	US-09-902-540-1262	Sequence 1262, Ap
	43	47.6	6.7	1221	4	US-09-252-991A-13701	Sequence 13701, A
C	44	47.6	6.7	1365	4	US-09-252-991A-13442	Sequence 13442, A
C	45	47.6	6.7	2337	4	US-09-252-991A-2034	Sequence 2034, Ap

Search completed: July 12, 2005, 18:32:49
Job time : 272.684 secs

                         GenCore version 5.1.6
                   Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 11:13:07 ;. Search time 1028.52 Seconds
                                          (without alignments)
                                          4315.680 Million cell updates/sec

Title: US-10-074-246-68
Perfect score: 707
Sequence: 1 tcgtagctggcttcctcgtc..........aaaaggcagtggaagcaaca 707

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 6330945 seqs, 3139162390 residues

Total number of hits satisfying chosen parameters: 12661890

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
                 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
                 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	707	100.0	707	14	US-10-074-246-68	Sequence 68, Appl
	2	705.4	99.8	881	14	US-10-074-246-58	Sequence 58, Appl
	3	426.6	60.3	691	14	US-10-074-246-62	Sequence 62, Appl
	4	411.8	58.2	698	14	US-10-074-246-63	Sequence 63, Appl
	5	383.8	54.3	685	14	US-10-074-246-70	Sequence 70, Appl
	6	376	53.2	686	14	US-10-074-246-69	Sequence 69, Appl
	7	370.8	52.4	802	14	US-10-074-246-65	Sequence 65, Appl
	8	369.2	52.2	628	14	US-10-074-246-66	Sequence 66, Appl
	9	350.6	49.6	785	14	US-10-074-246-61	Sequence 61, Appl
	10	344.2	48.7	712	14	US-10-074-246-64	Sequence 64, Appl
	11	330.2	46.7	642	14	US-10-074-246-59	Sequence 59, Appl
	12	312.6	44.2	745	14	US-10-074-246-60	Sequence 60, Appl
	13	236.4	33.4	729	14	US-10-074-246-71	Sequence 71, Appl
	14	139.4	19.7	216	14	US-10-074-246-57	Sequence 57, Appl
	15	138.2	19.5	9025608	15	US-10-156-761-1	Sequence 1, Appli
C	16	137.8	19.5	825	15	US-10-156-761-7462	Sequence 7462, Ap
C	17	89.6	12.7	816	15	US-10-156-761-581	Sequence 581, App
C	18	89.6	12.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
C	19	79	11.2	978	15	US-10-156-761-2643	Sequence 2643, Ap
C	20	78.4	11.1	9521	18	US-10-168-663-18	Sequence 18, Appl
	21	78.4	11.1	9521	18	US-10-168-663-19	Sequence 19, Appl
C	22	70.4	10.0	888	9	US-09-955-597-6	Sequence 6, Appli
C	23	70.4	10.0	12523	9	US-09-955-597-1	Sequence 1, Appli
C	24	67	9.5	1068	15	US-10-156-761-4239	Sequence 4239, Ap
C	25	66.8	9.4	927	15	US-10-156-761-3786	Sequence 3786, Ap
C	26	65.4	9.3	1185	9	US-09-894-844-71	Sequence 71, Appl
C	27	65.4	9.3	1185	17	US-10-388-902-71	Sequence 71, Appl
C	28	65.4	9.3	1185	18	US-10-647-089-71	Sequence 71, Appl
C	29	65.4	9.3	1188	17	US-10-282-122A-28727	Sequence 28727, A
C	30	64.4	9.1	825	10	US-09-953-348-58	Sequence 58, Appl
C	31	64.4	9.1	825	15	US-10-267-255-58	Sequence 58, Appl
	32	64.4	9.1	53500	10	US-09-953-348-76	Sequence 76, Appl
	33	64.4	9.1	53500	15	US-10-267-255-76	Sequence 76, Appl
C	34	62.8	8.9	927	15	US-10-156-761-6872	Sequence 6872, Ap
C	35	62.6	8.9	1287	15	US-10-156-761-832	Sequence 832, App
C	36	62	8.8	795	10	US-09-953-348-57	Sequence 57, Appl
C	37	62	8.8	795	15	US-10-267-255-57	Sequence 57, Appl
C	38	62	8.8	53500	10	US-09-953-348-76	Sequence 76, Appl
C	39	62	8.8	53500	15	US-10-267-255-76	Sequence 76, Appl
C	40	61.6	8.7	1101	15	US-10-156-761-2265	Sequence 2265, Ap
C	41	58	8.2	1719	15	US-10-156-761-3854	Sequence 3854, Ap
C	42	57.8	8.2	552	19	US-10-437-963-79213	Sequence 79213, A
C	43	57.8	8.2	1119	15	US-10-156-761-1197	Sequence 1197, Ap
C	44	56.4	8.0	3018	19	US-10-437-963-77223	Sequence 77223, A
C	45	56.4	8.0	11058	15	US-10-156-761-3629	Sequence 3629, Ap

Search completed: July 12, 2005, 20:49:00
Job time : 2703.52 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:06:45 ; Search time 5587.67 Seconds
                                          (without alignments)
                                          4816.222 Million cell updates/sec

Title: US-10-074-246-68
Perfect score: 707
Sequence: 1 tcgtagctggcttcctcgtc..........aaaaggcagtggaagcaaca 707

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est2:*
                3: gb_htc:*
                4: gb_est3:*
                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_gss1:*
                9: gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query
    No.   Score   Match Length DB   ID   Description

C   1   64.2   9.1   935   9   CNS006XK   AL066051 Drosophil
     2   63   8.9   925   9   CNS0091P   AL053013 Drosophil
C   3   62.2   8.8   925   9   CNS0091P   AL053013 Drosophil
     4   60.2   8.5   605   9   CC648836   CC648836 OGUJL60TV
C   5   60.2   8.5   873   9   CC682998   CC682998 OGWEA16TH
     6   58.8   8.3   935   9   CNS006XK   AL066051 Drosophil

	7	57	8.1	1542	9	AG032943	AG032943	Pan trogl
c	8	56.6	8.0	754	9	CC610065	CC610065	OGUJX42TV
c	9	56.4	8.0	1045	8	BZ564504	BZ564504	pacs2-164
c	10	56.4	8.0	2856	9	CL966856	CL966856	OsIFCC014
	11	56	7.9	932	9	CNS0072Q	AL066742	Drosophil
	12	55.8	7.9	849	9	CC718810	CC718810	OGLBV70TV
	13	55.8	7.9	859	8	CC328293	CC328293	OGOBE04TV
	14	55.8	7.9	929	9	CG290273	CG290273	OGZAU73TV
c	15	55.8	7.9	968	9	CG274354	CG274354	OG2BE18TV
c	16	55.4	7.8	822	9	CG290264	CG290264	OGZAU73TH
	17	55	7.8	502	8	BZ411257	BZ411257	OGAAC57TF
c	18	55	7.8	1307	9	CL486103	CL486103	SAIL_427_
c	19	54.6	7.7	552	9	CL980743	CL980743	OsIFCC045
c	20	54.6	7.7	552	9	CL980748	CL980748	OsIFCC045
	21	54.2	7.7	1152	9	AG076818	AG076818	Pan trogl
c	22	54	7.6	903	9	AG072453	AG072453	Pan trogl
c	23	53.4	7.6	1041	5	BQ652051	BQ652051	AGENCOURT
c	24	53.2	7.5	1009	9	CNS010EW	AL098882	Drosophil
c	25	52.4	7.4	1046	5	BQ643604	BQ643604	AGENCOURT
	26	52.4	7.4	1569	9	AG341503	AG341503	Mus muscu
	27	52.2	7.4	1319	9	CL498921	CL498921	SAIL_661_
c	28	51.6	7.3	762	9	CG308028	CG308028	OGVEH70TH
c	29	51.6	7.3	982	5	BQ687717	BQ687717	AGENCOURT
c	30	51.4	7.3	1399	8	BZ554759	BZ554759	pacs1-60_
c	31	51.2	7.2	931	7	CK412737	CK412737	AUF_IpGil
	32	50.8	7.2	414	8	BH630331	BH630331	1007088A0
c	33	50.8	7.2	638	9	CC657126	CC657126	OGDAG42TC
c	34	50.8	7.2	646	8	BZ974761	BZ974761	PUGJE03TB
	35	50.8	7.2	663	7	CF624053	CF624053	zmrws05_0
	36	50.8	7.2	718	8	BZ974765	BZ974765	PUGJE03TD
c	37	50.6	7.2	932	9	CNS0072Q	AL066742	Drosophil
c	38	50.4	7.1	1375	2	AW727483	AW727483	GA__Ea001
c	39	50.4	7.1	1473	9	CL975386	CL975386	OsIFCC027
c	40	50.2	7.1	776	9	CNS010RY	AL099352	Drosophil
c	41	50.2	7.1	839	9	CNS004NB	AL054280	Drosophil
c	42	50	7.1	557	5	BU037493	BU037493	946139F05
c	43	50	7.1	589	5	BQ778943	BQ778943	946115F10
c	44	50	7.1	688	6	CA830993	CA830993	1117014B0
	45	49.8	7.0	411	8	AQ961051	AQ961051	LERFI83TR

Sequence: 1 gccgtccagtcgttaatgtcgc 22

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                   1: gb_ba:*
                   2: gb_htg:*
                   3: gb_in:*
                   4: gb_om:*
                   5: gb_ov:*
                   6: gb_pat:*
                   7: gb_ph:*
                   8: gb_pl:*
                   9: gb_pr:*
                   10: gb_ro:*
                   11: gb_sts:*
                   12: gb_sy:*
                   13: gb_un:*
                   14: gb_vi:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                                  SUMMARIES

                     %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
      1   22   100.0   22   6   BD171663   BD171663 Identific
      2   22   100.0   22   6   AX278539   AX278539 Sequence
      3   22   100.0   22   6   AX513096   AX513096 Sequence
      4   22   100.0   24   6   AX513119   AX513119 Sequence
      5   22   100.0   323   6   BD171699   BD171699 Identific
      6   22   100.0   369   6   BD171700   BD171700 Identific
      7   22   100.0   611   6   BD171688   BD171688 Identific
      8   22   100.0   611   6   BD171689   BD171689 Identific
      9   22   100.0   628   6   AX513137   AX513137 Sequence
     10   22   100.0   802   6   AX513136   AX513136 Sequence
     11   22   100.0 110000   1   AE000516_10   Continuation (11 o
     12   22   100.0 327650   1   BX248337   BX248337 Mycobacte
     13   22   100.0 349306   1   BX842575   BX842575 Mycobacte
     14   19   86.4   19   6   AX513123   AX513123 Sequence
c   15   18.8   85.5   3276   6   A44223   A44223 Sequence 4
c   16   18.8   85.5   3276   6   A72710   A72710 Sequence 4

c	17	18.8	85.5	3276	6	AR408850	AR408850 Sequence
c	18	18.8	85.5	3276	6	AX002862	AX002862 Sequence
c	19	18.8	85.5	4314	8	GLEY18738	Y18738 Gracilariop
c	20	17.8	80.9	214922	2	AC150991	AC150991 Bos tauru
c	21	17.8	80.9	226889	14	AC146905	AC146905 Human Her
c	22	17.8	80.9	229209	14	AC146907	AC146907 Human Her
	23	17.8	80.9	229354	6	AR474465	AR474465 Sequence
	24	17.8	80.9	229354	6	AR475529	AR475529 Sequence
	25	17.8	80.9	229354	6	AX686187	AX686187 Sequence
	26	17.8	80.9	229354	14	HEHCMVCG	X17403 Human cytom
	27	17.8	80.9	229483	14	AC146851	AC146851 Human Her
c	28	17.8	80.9	229700	14	AC146904	AC146904 Human Her
	29	17.8	80.9	231236	14	AY315197	AY315197 Human her
c	30	17.8	80.9	233739	14	AC146999	AC146999 Human Her
	31	17.8	80.9	234881	14	AC146906	AC146906 Human Her
	32	17.8	80.9	235645	14	AY446894	AY446894 Human her
c	33	17.2	78.2	97095	2	AC141824	AC141824 Apis mell
c	34	17.2	78.2	160042	2	AL365211	AL365211 Homo sapi
	35	17.2	78.2	175968	9	AC018684	AC018684 Homo sapi
c	36	17.2	78.2	300425	1	AP005022	AP005022 Streptomy
	37	17.2	78.2	302070	1	AP005223	AP005223 Corynebac
	38	16.8	76.4	70290	2	AC100833	AC100833 Homo sapi
	39	16.8	76.4	105689	2	AC136152	AC136152 Rattus no
	40	16.8	76.4	110000	1	U00096_02	Continuation (3 of
c	41	16.8	76.4	113253	·2	AC092356	AC092356 Homo sapi
	42	16.8	76.4	128824	1	ECU73857	U73857 Escherichia
	43	16.8	76.4	155862	9	AC018464	AC018464 Homo sapi
c	44	16.8	76.4	156349	10	AC117550	AC117550 Mus muscu
	45	16.8	76.4	162167	2	AC019271	AC019271 Homo sapi

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 26.3482 Seconds
                                          (without alignments)
                                          4942.816 Million cell updates/sec

Title: US-10-074-246-25
Perfect score: 22
Sequence: 1 gccgtccagtcgttaatgtcgc 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   22   100.0   22   6   ABS70044   Abs70044 Mycobacte
     2   22   100.0   22   6   ABA81861   Aba81861 M tubercu
     3   22   100.0   22   8   ABX10101   Abx10101 M. tuberc
     4   22   100.0   24   6   ABS70067   Abs70067 Mycobacte
     5   22   100.0   628   6   ABS70085   Abs70085 Mycobacte

	6	22	100.0	628	8	ABX10111	Abx10111 M. bovis
	7	22	100.0	648	8	ABX10126	Abx10126 M. tuberc
	8	22	100.0	648	8	ABX10127	Abx10127 M. bovis
	9	22	100.0	802	6	ABS70084	Abs70084 Mycobacte
	10	22	100.0	802	8	ABX10110	Abx10110 M. tuberc
	11	22	100.0	110000	4	AAI99682_10	Continuation (11 o
	12	22	100.0	110000	4	AAI99683_10	Continuation (11 o
	13	19	86.4	19	6	ABS70071	Abs70071 Mycobacte
c	14	18.8	85.5	3276	2	AAQ88050	Aaq88050 Glucan Ly
c	15	18.8	85.5	3276	2	AAQ87604	Aaq87604 Fungus-in
c	16	18.8	85.5	3276	2	AAV84193	Aav84193 Gracilari
	17	17.8	80.9	229354	6	ABQ74179	Abq74179 Human cyt
	18	17.4	79.1	43011	12	ADN01941	Adn01941 Staphyloc
c	19	17.2	78.2	907	8	ABZ52394	Abz52394 Aspergill
c	20	16.8	76.4	2383	5	AAS89875	Aas89875 DNA encod
c	21	16.8	76.4	2451	5	AAS85748	Aas85748 DNA encod
c	22	15.8	71.8	417	8	ABZ52746	Abz52746 Aspergill
c	23	15.8	71.8	617	3	AAF08207	Aaf08207 Fusarium
c	24	15.8	71.8	1044	10	ABZ66697	Abz66697 Orthosomy
	25	15.8	71.8	1140	6	ABQ22020	Abq22020 Oligonucl
c	26	15.8	71.8	1140	6	ABQ22021	Abq22021 Oligonucl
	27	15.8	71.8	1362	4	AAF60956	Aaf60956 P. putida
c	28	15.8	71.8	1377	8	ACA53865	Aca53865 Prokaryot
c	29	15.8	71.8	1410	10	ADG33797	Adg33797 Actinomyc
c	30	15.8	71.8	2000	8	ADA71563	Ada71563 Rice gene
	31	15.8	71.8	3738	8	ACA36064	Aca36064 Prokaryot
	32	15.8	71.8	3849	11	ACH96678	Ach96678 Klebsiell
c	33	15.8	71.8	4316	10	ADB69197	Adb69197 C. neofor
	34	15.8	71.8	37116	10	ABZ66810	Abz66810 Orthosomy
c	35	15.8	71.8	109519	5	AAS08693 ·	Aas08693 Micromono
c	36	15.8	71.8	110000	10	ADF77343_08	Continuation (9 of
	37	15.6	70.9	348	11	ABD15073	Abd15073 Pseudomon
	38	15.6	70.9	690	6	ABQ24858	Abq24858 Oligonucl
c	39	15.6	70.9	690	6	ABQ24859	Abq24859 Oligonucl
c	40	15.6	70.9	852	4	AAK91722	Aak91722 Human cDN
c	41	15.6	70.9	852	4	AAK93988	Aak93988 Human cDN
c	42	15.6	70.9	852	12	ADL28149	Adl28149 5' end of
c	43	15.6	70.9	852	12	ADL30415	Adl30415 5' end of
	44	15.6	70.9	925	13	ADS56904	Ads56904 Bacterial
	45	15.6	70.9	1086	12	ADO48504	Ado48504 Human 108

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:18:20 ; Search time 7.76952 Seconds
                                           (without alignments)
                                         , 4633.247 Million cell updates/sec

Title: US-10-074-246-25
Perfect score: 22
Sequence: 1 gccgtccagtcgttaatgtcgc 22

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

                         %
Result   .   Query
     No.   Score Match Length DB   ID   Description
    ----
       1   22 100.0 4403765 3   US-09-103-840A-2   Sequence 2, Appli
       2   22 100.0 4411529 3   US-09-103-840A-1   Sequence 1, Appli
  c   3   18.8   85.5   3276 3   US-08-633-768A-4   Sequence 4, Appli
  c   4   18.8   85.5   3276 4   US-09-280-197-4   Sequence 4, Appli
       5   17.8   80.9 229354 4   US-09-705-400-64   Sequence 64, Appl
  c   6   16.8   76.4   1305 4   US-09-902-540-4277   Sequence 4277, Ap
       7   16.8   76.4   26012 4   US-09-902-540-1212   Sequence 1212, Ap
  c   8   16.2   73.6   1145 3   US-09-221-017B-944   Sequence 944, App
  c   9   16.2   73.6   4800 4   US-09-902-540-562   Sequence 562, App
  c   10   16   72.7   765 4   US-09-248-796A-1849   Sequence 1849, Ap
      11   15.8   71.8   3849 4   US-09-489-039A-2473   Sequence 2473, Ap
      12   15.6   70.9   348 4   US-09-252-991A-13677   Sequence 13677, A

	13	15.6	70.9	486	4	US-09-902-540-3038	Sequence 3038, Ap
	14	15.6	70.9	1557	3	US-07-852-132A-12	Sequence 12, Appl
	15	15.6	70.9	1557	5	PCT-US91-01327-12	Sequence 12, Appl
	16	15.6	70.9	1557	6	5248670-2	Patent No. 5248670
	17	15.6	70.9	1557	6	5248670-2	Patent No. 5248670
	18	15.6	70.9	1623	4	US-09-489-039A-88	Sequence 88, Appl
	19	15.6	70.9	1992	4	US-09-252-991A-13771	Sequence 13771, A
c	20	15.6	70.9	2175	4	US-09-252-991A-13657	Sequence 13657, A
c	21	15.6	70.9	2292	4	US-09-252-991A-13575	Sequence 13575, A
c	22	15.6	70.9	3279	4	US-09-275-608-1	Sequence 1, Appli
	23	15.6	70.9	5105	4	US-09-902-540-791	Sequence 791, App
c	24	15.6	70.9	27219	4	US-09-902-540-1244	Sequence 1244, Ap
	25	15.6	70.9	87563	3	US-09-453-702B-57	Sequence 57, Appl
c	26	15.6	70.9	154746	4	US-09-827-688-8	Sequence 8, Appli
	27	15.2	69.1	601	4	US-09-949-016-206008	Sequence 206008,
	28	15.2	69.1	601	4	US-09-949-016-206009	Sequence 206009,
c	29	15.2	69.1	792	4	US-09-976-594-511	Sequence 511, App
	30	15.2	69.1	851	3	US-09-008-892-10	Sequence 10, Appl
c	31	15.2	69.1	897	4	US-09-902-540-7777	Sequence 7777, Ap
	32	15.2	69.1	6250	4	US-09-902-540-773	Sequence 773, App
	33	15.2	69.1	100990	4	US-09-409-800B-2	Sequence 2, Appli
c	34	15.2	69.1	116966	4	US-09-949-016-17557	Sequence 17557, A
c	35	15.2	69.1	229354	4	US-09-705-400-64	Sequence 64, Appl
c	36	15	68.2	1572	4	US-09-489-039A-5714	Sequence 5714, Ap
c	37	14.8	67.3	927	1	US-08-499-568-1	Sequence 1, Appli
c	38	14.8	67.3	927	1	US-08-793-958-1	Sequence 1, Appli
c	39	14.8	67.3	930	4	US-09-134-000C-3208	Sequence 3208, Ap
c	40	14.8	67.3	1180	4	US-09-247-890-2	Sequence 2, Appli
c	41	14.8	67.3	1180	4	US-09-724-969-2	Sequence 2, Appli
c	42	14.8	67.3	1180	4	US-09-724-852-2	Sequence 2, Appli
c	43	14.8	67.3	1185	4	US-09-247-890-1	Sequence 1, Appli
c	44	14.8	67.3	1185	4	US-09-724-969-1	Sequence 1, Appli
c	45	14.8	67.3	1185	4	US-09-724-852-1	Sequence 1, Appli

GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 11:13:07 ; Search time 32.005 Seconds
                                            (without alignments)
                                            4315.680 Million cell updates/sec

Title: US-10-074-246-25
Perfect score: 22
Sequence: 1 gccgtccagtcgttaatgtcgc 22

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 6330945 seqs, 3139162390 residues

Total number of hits satisfying chosen parameters: 12661890

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                  1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                  2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                  3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                  4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                  5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                  6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                  7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                  8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                  9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                  10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                  11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                  12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                  13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                  14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                  15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                  16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                  17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                  18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                  19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                  20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
                  21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
                  22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                  23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                  24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                  25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                  26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

    Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	22	100.0	22	9	US-09-817-014-72	Sequence 72, Appl
	2	22	100.0	22	14	US-10-074-246-25	Sequence 25, Appl
	3	22	100.0	22	16	US-10-056-229-72	Sequence 72, Appl
	4	22	100.0	24	14	US-10-074-246-48	Sequence 48, Appl
	5	22	100.0	628	14	US-10-074-246-66	Sequence 66, Appl
	6	22	100.0	802	14	US-10-074-246-65	Sequence 65, Appl
	7	19	86.4	19	14	US-10-074-246-52	Sequence 52, Appl
C	8	18.8	85.5	3276	9	US-09-280-197-4	Sequence 4, Appli
C	9	18.8	85.5	3276	9	US-09-423-126-8	Sequence 8, Appli
C	10	18.8	85.5	3276	17	US-10-448-139-4	Sequence 4, Appli
C	11	18.8	85.5	3276	21	US-10-879-638-8	Sequence 8, Appli
	12	17.8	80.9	218802	21	US-10-897-508-1	Sequence 1, Appli
C	13	17.2	78.2	9025608	15	US-10-156-761-1	Sequence 1, Appli
	14	16.4	74.5	743	20	US-10-425-115-173257	Sequence 173257,
C	15	16.2	73.6	408	20	US-10-425-115-112345	Sequence 112345,
C	16	16.2	73.6	1145	13	US-10-194-163-944	Sequence 944, App
C	17	16.2	73.6	1380	15	US-10-156-761-5958	Sequence 5958, Ap
C	18	16.2	73.6	2078	20	US-10-425-115-51743	Sequence 51743, A
C	19	16.2	73.6	2085	20	US-10-739-930-2710	Sequence 2710, Ap
	20	15.8	71.8	25	21	US-10-719-900-182550	Sequence 182550,
C	21	15.8	71.8	416	20	US-10-425-115-5185	Sequence 5185, Ap
C	22	15.8	71.8	617	20	US-10-653-047-730	Sequence 730, App
C	23	15.8	71.8	1041	11	US-09-758-759-12	Sequence 12, Appl
C	24	15.8	71.8	1044	17	US-10-107-431-56	Sequence 56, Appl
	25	15.8	71.8	1140	20	US-10-363-345A-8611	Sequence 8611, Ap
C	26	15.8	71.8	1140	20	US-10-363-345A-8612	Sequence 8612, Ap
	27	15.8	71.8	1140	21	US-10-363-483A-8611	Sequence 8611, Ap
C	28	15.8	71.8	1140	21	US-10-363-483A-8612	Sequence 8612, Ap
C	29	15.8	71.8	1377	17	US-10-282-122A-41735	Sequence 41735, A
C	30	15.8	71.8	1410	18	US-10-417-700A-56	Sequence 56, Appl
	31	15.8	71.8	3738	17	US-10-282-122A-23934	Sequence 23934, A
C	32	15.8	71.8	4316	17	US-10-320-797-324	Sequence 324, App
	33	15.8	71.8	37116	17	US-10-107-431-279	Sequence 279, App
C	34	15.8	71.8	109519	11	US-09-758-759-1	Sequence 1, Appli
C	35	15.6	70.9	25	21	US-10-719-900-527126	Sequence 527126,
C	36	15.6	70.9	118	20	US-10-425-115-150443	Sequence 150443,
C	37	15.6	70.9	294	20	US-10-425-115-70317	Sequence 70317, A
C	38	15.6	70.9	510	20	US-10-425-115-125969	Sequence 125969,
	39	15.6	70.9	624	20	US-10-425-115-23654	Sequence 23654, A
	40	15.6	70.9	690	20	US-10-363-345A-11449	Sequence 11449, A
C	41	15.6	70.9	690	20	US-10-363-345A-11450	Sequence 11450, A
	42	15.6	70.9	690	21	US-10-363-483A-11449	Sequence 11449, A
C	43	15.6	70.9	690	21	US-10-363-483A-11450	Sequence 11450, A
	44	15.6	70.9	925	17	US-10-369-493-32578	Sequence 32578, A
C	45	15.6	70.9	1358	18	US-10-424-599-35716	Sequence 35716, A

GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:06:45 ; Search time 173.874 Seconds
                                            (without alignments)
                                            4816.222 Million cell updates/sec

Title: US-10-074-246-25
Perfect score: 22
Sequence: 1 gccgtccagtcgttaatgtcgc 22

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est2:*
                3: gb_htc:*
                4: gb_est3:*
                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_gss1:*
                9: gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
    No.   Score   Match Length DB   ID   Description

C   1   19.4   88.2   497   7   CK101783   CK101783 F118P27.5
    2   17.8   80.9   452   6   CF026765   CF026765 QCB11f12.
C   3   17.8   80.9   1143   9   AG175746   AG175746 Pan trogl
C   4   17.2   78.2   402   7   CO134696   CO134696 EST829367
C   5   17.2   78.2   428   7   CO137596   CO137596 EST832267
C   6   17.2   78.2   557   8   AZ396799   AZ396799 1M0161E03
C   7   17.2   78.2   664   9   AG180620   AG180620 Pan trogl
    8   17.2   78.2   852   7   CK416341   CK416341 AUF_IpInt
    9   17.2   78.2   879   8   AQ271729   AQ271729 nbxb0026J

c	10	17.2	78.2	949	9	CNS070DV	AL423497	T7 end of
	11	17	77.3	894	9	CNS03HB0	AL244053	Tetraodon
	12	16.8	76.4	331	8	AZ719254	AZ719254	RPCI-24-1
c	13	16.8	76.4	341	8	AZ620126	AZ620126	1M0452P10
	14	16.8	76.4	433	8	AZ716289	AZ716289	RPCI-24-1
	15	16.8	76.4	547	8	AZ901323	AZ901323	RPCI-24-1
	16	16.8	76.4	806	8	AZ717730	AZ717730	RPCI-24-1
c	17	16.8	76.4	1350	9	AG398251	AG398251	Mus muscu
c	18	16.8	76.4	1649	9	AG098046	AG098046	Pan trogl
c	19	16.4	74.5	215	4	BG349271	BG349271	947030B12
c	20	16.4	74.5	363	4	BG349270	BG349270	947030B12
c	21	16.4	74.5	416	7	CO524986	CO524986	3530_1_16
c	22	16.4	74.5	431	4	BI273510	BI273510	949026E12
	23	16.4	74.5	448	5	BX765912	BX765912	BX765912
c	24	16.4	74.5	472	6	CB278998	CB278998	ru39d09.y
c	25	16.4	74.5	515	4	BM499183	BM499183	947043D01
c	26	16.4	74.5	529	4	BG360883	BG360883	947043D01
	27	16.4	74.5	532	4	BI319172	BI319172	949026E12
c	28	16.4	74.5	536	9	TA31E07Q	AL454323	T. brucei
c	29	16.4	74.5	552	6	CA141332	CA141332	SCJFRT205
c	30	16.4	74.5	552	7	CO534599	CO534599	3530_1_22
c	31	16.4	74.5	555·	4	BI992275	BI992275	1020058H0
c	32	16.4	74.5	624	8	AQ651426	AQ651426	Sheared D
c	33	16.4	74.5	917	3	CNS09ENE	BX055062	Single re
	34	16.4	74.5	918	8	AZ211507	AZ211507	SP_0155_B
c	35	16.4	74.5	1025	7	CF879123	CF879123	tric019xh
	36	16.2	73.6	293	8	AQ645354	AQ645354	RPCI93-Ec
c	37·	16.2	73.6	303	2	BB498742	BB498742	BB498742
c	38	16.2	73.6	335	2	AW969377	AW969377	EST381454
c	39	16.2	73.6	354	5	BQ488000	BQ488000	10-E8249-
c	40	16.2	73.6	356	2	BE614894	BE614894	601280320
	41	16.2	73.6	357	8	CC446822	CC446822	PUHBA36TD
c	42	16.2	73.6	392	8	AZ214685	AZ214685	Sheared D
c	43	16.2	73.6	420	1.	AJ486483	AJ486483	AJ486483
c	44	16.2	73.6	441	4	BJ472984	BJ472984	BJ472984
	45	16.2	73.6	450	7	CO640664	CO640664	USDA-FP_1

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 164.059 Seconds
                                        (without alignments)
                                        7088.436 Million cell updates/sec

Title: US-10-074-246-48
Perfect score: 24
Sequence: 1 cggccgtccagtcgttaatgtcgc 24

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                1: gb_ba:*
                2: gb_htg:*
                3: gb_in:*
                4: gb_om:*
                5: gb_ov:*
                6: gb_pat:*
                7: gb_ph:*
                8: gb_pl:*
                9: gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
  No.   Score Match Length DB ID   Description
----
      1   24 100.0   24 6 AX513119   AX513119 Sequence
      2   24 100.0   323 6 BD171699   BD171699 Identific
      3   24 100.0   369 6 BD171700   BD171700 Identific

c	#						
	4	24	100.0	611	6	BD171688	BD171688 Identific
	5	24	100.0	611	6	BD171689	BD171689 Identific
	6	24	100.0	628	6	AX513137	AX513137 Sequence
	7	24	100.0	802	6	AX513136	AX513136 Sequence
	8	24	100.0	110000	1	AE000516_10	Continuation (11 o
	9	24	100.0	327650	1	BX248337	BX248337 Mycobacte
	10	24	100.0	349306	1	BX842575	BX842575 Mycobacte
	11	22	91.7	22	6	BD171663	BD171663 Identific
	12	22	91.7	22	6	AX278539	AX278539 Sequence
	13	22	91.7	22	6	AX513096	AX513096 Sequence
c	14	19.2	80.0	300425	1	AP005022	AP005022 Streptomy
	15	19	79.2	19	6	AX513123	AX513123 Sequence
c	16	18.8	78.3	3276	6	A44223	A44223 Sequence 4
c	17	18.8	78.3	3276	6	A72710	A72710 Sequence 4
c	18	18.8	78.3	3276	6	AR408850	AR408850 Sequence
c	19	18.8	78.3	3276	6	AX002862	AX002862 Sequence
c	20	18.8	78.3	4314	8	GLEY18738	Y18738 Gracilariop
c	21	18.2	75.8	11533	1	AE009124	AE009124 Agrobacte
c	22	18.2	75.8	12074	1	AE008089	AE008089 Agrobacte
c	23	18.2	75.8	160042	2	AL365211	AL365211 Homo sapi
	24	18.2	75.8	175968	9	AC018684	AC018684 Homo sapi
c	25	18.2	75.8	226889	14	AC146905	AC146905 Human Her
c	26	18.2	75.8	229209	14	AC146907	AC146907 Human Her
	27	18.2	75.8	229354	6	AR474465	AR474465 Sequence
	28	18.2	75.8	229354	6	AR475529	AR475529 Sequence
	29	18.2	75.8	229354	6	AX686187	AX686187 Sequence
	30	18.2	75.8	229354	14	HEHCMVCG	X17403 Human cytom
	31	18.2	75.8	229483	14	AC146851	AC146851 Human Her
c	32	18.2	75.8	229700	14	AC146904	AC146904 Human Her
	33	18.2	75.8	231236	14	AY315197	AY315197 Human her
c	34	18.2	75.8	233739	14	AC146999	AC146999 Human Her
	35	18.2	75.8	234881	14	AC146906	AC146906 Human Her
	36	18.2	75.8	235645	14	AY446894	AY446894 Human her
	37	18.2	75.8	302070	1	AP005223	AP005223 Corynebac
c	38	17.8	74.2	42730	3	CEC23H4	Z78416 Caenorhabdi
	39	17.8	74.2	162167	2	AC019271	AC019271 Homo sapi
c	40	17.8	74.2	162167	2	AC019271	AC019271 Homo sapi
c	41	17.8	74.2	181497	9	AC096670	AC096670 Homo sapi
c	42	17.8	74.2	214922	2	AC150991	AC150991 Bos tauru
c	43	17.6	73.3	700	9	HSA329475	AJ329475 Homo sapi
	44	17.6	73.3	959	3	AF047615	AF047615 Euroglyph
c	45	17.6	73.3	1319	1	ATIS426	X56562 A.tumefacie

```
Perfect score:    24
Sequence:         1 cggccgtccagtcgttaatgtcgc 24

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:        8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        N_Geneseq_16Dec04:*
                  1:  geneseqn1980s:*
                  2:  geneseqn1990s:*
                  3:  geneseqn2000s:*
                  4:  geneseqn2001as:*
                  5:  geneseqn2001bs:*
                  6:  geneseqn2002as:*
                  7:  geneseqn2002bs:*
                  8:  geneseqn2003as:*
                  9:  geneseqn2003bs:*
                  10:  geneseqn2003cs:*
                  11:  geneseqn2003ds:*
                  12:  geneseqn2004as:*
                  13:  geneseqn2004bs:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24	100.0	24	6	ABS70067	Abs70067 Mycobacte
	2	24	100.0	628	6	ABS70085	Abs70085 Mycobacte
	3	24	100.0	628	8	ABX10111	Abx10111 M. bovis
	4	24	100.0	648	8	ABX10126	Abx10126 M. tuberc
	5	24	100.0	648	8	ABX10127	Abx10127 M. bovis
	6	24	100.0	802	6	ABS70084	Abs70084 Mycobacte
	7	24	100.0	802	8	ABX10110	Abx10110 M. tuberc
	8	24	100.0	110000	4	AAI99682_10	Continuation (11 o
	9	24	100.0	110000	4	AAI99683_10	Continuation (11 o
	10	22	91.7	22	6	ABS70044	Abs70044 Mycobacte
	11	22	91.7	22	6	ABA81861	Aba81861 M tubercu
	12	22	91.7	22	8	ABX10101	Abx10101 M. tuberc
	13	19	79.2	19	6	ABS70071	Abs70071 Mycobacte
c	14	18.8	78.3	3276	2	AAQ88050	Aaq88050 Glucan Ly
c	15	18.8	78.3	3276	2	AAQ87604	Aaq87604 Fungus-in
c	16	18.8	78.3	3276	2	AAV84193	Aav84193 Gracilari

	17	18.2	75.8	229354	6	ABQ74179	Abq74179 Human cyt
c	18	17.6	73.3	907	8	ABZ52394	Abz52394 Aspergill
c	19	17.6	73.3	1989	3	AAC64054	Aac64054 Winter wh
c	20	17.6	73.3	2006	2	AAQ50147	Aaq50147 Phospholi
c	21	17.6	73.3	20000	9	ADA00836	Ada00836 Agrobacte
	22	17.6	73.3	86248	10	ADC00087	Adc00087 Enterohae
	23	17.6	73.3	87563	9	ACD19044	Acd19044 E. coli 0
	24	17.6	73.3	110000	4	AAI99682_36	Continuation (37 o
	25	17.6	73.3	110000	4	AAI99683_36	Continuation (37 o
c	26	17.4	72.5	216	10	ADE52337	Ade52337 Norway ra
c	27	17.4	72.5	216	10	ADH56123	Adh56123 Rat pain-
	28	17.4	72.5	43011	12	ADN01941	Adn01941 Staphyloc
c	29	17.2	71.7	1416	4	ABL11553	Abl11553 Drosophil
	30	17.2	71.7	4045	4	ABL11552	Abl11552 Drosophil
c	31	16.8	70.0	2383	5	AAS89875	Aas89875 DNA encod
c	32	16.8	70.0	2451	5	AAS85748	Aas85748 DNA encod
	33	16.6	69.2	1425	5	AAH68448	Aah68448 C glutami
	34	16.6	69.2	1554	4	AAF71396	Aaf71396 Corynebac
c	35	16.6	69.2	2787	6	ABK88156	Abk88156 Alpha-iso
c	36	16.6	69.2	5811	6	ABK88159	Abk88159 DNA encod
c	37	16.6	69.2	5811	8	ADA26477	Ada26477 Alpha-iso
c	38	16.6	69.2	6153	8	ADA26478	Ada26478 Alpha-iso
	39	16.6	69.2	8446	6	ADG79370	Adg79370 Human sec
c	40	16.6	69.2	11705	2	AAV62160	Aav62160 HSV-2 str
c	41	16.6	69.2	12700	2	AAV62133	Aav62133 HSV-2 str
	42	16.6	69.2	37286	4	AAS59522	Aas59522 Propionib
	43	16.6	69.2	37286	8	ACF64451	Acf64451 Propionib
c	44	16.6	69.2	85692	12	ADI39159	Adi39159 Streptomy
c	45	16.6	69.2	117213	2	AAV62176	Aav62176 HSV-2 str

GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:18:20 ; Search time 8.47584 Seconds
                                            (without alignments)
                                            4633.247 Million cell updates/sec

Title: US-10-074-246-48
Perfect score: 24
Sequence: 1 cggccgtccagtcgttaatgtcgc 24

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
2	24	100.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 3	18.8	78.3	3276	3	US-08-633-768A-4	Sequence 4, Appli
c 4	18.8	78.3	3276	4	US-09-280-197-4	Sequence 4, Appli
c 5	18.2	75.8	4800	4	US-09-902-540-562	Sequence 562, App
6	18.2	75.8	229354	4	US-09-705-400-64	Sequence 64, Appl
7	17.6	73.3	87563	3	US-09-453-702B-57	Sequence 57, Appl
c 8	17.2	71.7	1305	4	US-09-902-540-4277	Sequence 4277, Ap
9	17.2	71.7	26012	4	US-09-902-540-1212	Sequence 1212, Ap
10	16.6	69.2	486	4	US-09-902-540-3038	Sequence 3038, Ap
c 11	16.6	69.2	1145	3	US-09-221-017B-944	Sequence 944, App
12	16.6	69.2	1557	3	US-07-852-132A-12	Sequence 12, Appl

	13	16.6	69.2	1557	5	PCT-US91-01327-12	Sequence 12, Appl
	14	16.6	69.2	1557	6	5248670-2	Patent No. 5248670
	15	16.6	69.2	1557	6	5248670-2	Patent No. 5248670
	16	16.6	69.2	5105	4	US-09-902-540-791	Sequence 791, App
c	17	16.6	69.2	154746	4	US-09-827-688-8	Sequence 8, Appli
c	18	16.2	67.5	601	4	US-09-949-016-23060	Sequence 23060, A
c	19	16.2	67.5	601	4	US-09-949-016-188517	Sequence 188517,
c	20	16.2	67.5	2643	4	US-09-902-540-2841	Sequence 2841, Ap
c	21	16.2	67.5	2883	4	US-09-949-016-5388	Sequence 5388, Ap
c	22	16.2	67.5	2923	1	US-08-377-292-6	Sequence 6, Appli
c	23	16.2	67.5	2923	2	US-07-989-847-7	Sequence 7, Appli
c	24	16.2	67.5	2923	3	US-08-469-411-7	Sequence 7, Appli
c	25	16.2	67.5	2923	4	US-09-780-601A-7	Sequence 7, Appli
c	26	16.2	67.5	2923	6	5187076-5	Patent No. 5187076
c	27	16.2	67.5	2923	6	5187076-5	Patent No. 5187076
c	28	16.2	67.5	2943	4	US-09-949-016-247	Sequence 247, App
	29	16.2	67.5	16047	4	US-09-902-540-1136	Sequence 1136, Ap
c	30	16.2	67.5	158735	4	US-09-949-016-11989	Sequence 11989, A
c	31	16.2	67.5	158735	4	US-09-949-016-17130	Sequence 17130, A
c	32	16	66.7	409	4	US-09-902-540-5238	Sequence 5238, Ap
c	33	16	66.7	549	1	US-08-361-467B-10	Sequence 10, Appl
c	34	16	66.7	549	1	US-08-484-332C-10	Sequence 10, Appl
c	35	16	66.7	615	3	US-08-357-497-3	Sequence 3, Appli
c	36	16	66.7	615	4	US-09-794-384A-6	Sequence 6, Appli
c	37	16	66.7	765	4	US-09-248-796A-1849	Sequence 1849, Ap
c	38	16	66.7	790	3	US-09-363-970-4	Sequence 4, Appli
c	39	16	66.7	1989	4	US-09-534-228B-6	Sequence 6, Appli
	40	16	66.7	2101	4	US-09-902-540-3956	Sequence 3956, Ap
c	41	16	66.7	2345	3	US-09-026-673-1	Sequence 1, Appli
c	42	16	66.7	2345	3	US-09-512-650-1	Sequence 1, Appli
c	43	16	66.7	2345	3	US-09-480-142-1	Sequence 1, Appli
c	44	16	66.7	2345	4	US-09-573-555-2	Sequence 2, Appli
c	45	16	66.7	3544	2	US-08-485-139-3	Sequence 3, Appli

GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 11:13:07 ; Search time 34.9145 Seconds
                                            (without alignments)
                                            4315.680 Million cell updates/sec

Title: US-10-074-246-48
Perfect score: 24
Sequence: 1 cggccgtccagtcgttaatgtcgc 24

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 6330945 seqs, 3139162390 residues

Total number of hits satisfying chosen parameters: 12661890

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                  1:   /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                  2:   /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                  3:   /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                  4:   /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                  5:   /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                  6:   /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                  7:   /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                  8:   /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                  9:   /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                  10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                  11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                  12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                  13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                  14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                  15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                  16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                  17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                  18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                  19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                  20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
                  21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
                  22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                  23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                  24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                  25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                  26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24	100.0	24	14	US-10-074-246-48	Sequence 48, Appl
	2	24	100.0	628	14	US-10-074-246-66	Sequence 66, Appl
	3	24	100.0	802	14	US-10-074-246-65	Sequence 65, Appl
	4	22	91.7	22	9	US-09-817-014-72	Sequence 72, Appl
	5	22	91.7	22	14	US-10-074-246-25	Sequence 25, Appl
	6	22	91.7	22	16	US-10-056-229-72	Sequence 72, Appl
C	7	19.2	80.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
	8	19	79.2	19	14	US-10-074-246-52	Sequence 52, Appl
C	9	18.8	78.3	3276	9	US-09-280-197-4	Sequence 4, Appli
C	10	18.8	78.3	3276	9	US-09-423-126-8	Sequence 8, Appli
C	11	18.8	78.3	3276	17	US-10-448-139-4	Sequence 4, Appli
C	12	18.8	78.3	3276	21	US-10-879-638-8	Sequence 8, Appli
	13	18.2	75.8	218802	21	US-10-897-508-1	Sequence 1, Appli
C	14	17.6	73.3	416	20	US-10-425-115-5185	Sequence 5185, Ap
	15	17.6	73.3	2163	19	US-10-437-963-15518	Sequence 15518, A
C	16	17.6	73.3	20000	10	US-09-992-009-1	Sequence 1, Appli
	17	17.6	73.3	87563	14	US-10-114-170-57	Sequence 57, Appl
C	18	17.4	72.5	216	17	US-10-368-819-50	Sequence 50, Appl
C	19	17.2	71.7	1380	15	US-10-156-761-5958	Sequence 5958, Ap
C	20	16.6	69.2	25	21	US-10-719-900-527126	Sequence 527126,
	21	16.6	69.2	1098	15	US-10-156-761-434	Sequence 434, App
C	22	16.6	69.2	1145	13	US-10-194-163-944	Sequence 944, App
	23	16.6	69.2	1425	9	US-09-738-626-3483	Sequence 3483, Ap
	24	16.6	69.2	1554	19	US-10-781-014-73	Sequence 73, Appl
C	25	16.6	69.2	1554	20	US-10-425-115-13416	Sequence 13416, A
C	26	16.6	69.2	2787	19	US-10-466-085A-6	Sequence 6, Appli
C	27	16.6	69.2	5811	19	US-10-466-085A-32	Sequence 32, Appl
C	28	16.6	69.2	85692	18	US-10-461-194-1	Sequence 1, Appli
C	29	16.6	69.2	154746	10	US-09-827-688-8	Sequence 8, Appli
C	30	16.6	69.2	3309400	9	US-09-738-626-1	Sequence 1, Appli
	31	16.4	68.3	743	20	US-10-425-115-173257	Sequence 173257,
C	32	16.2	67.5	25	21	US-10-956-157-174238	Sequence 174238,
C	33	16.2	67.5	25	21	US-10-956-157-216105	Sequence 216105,
C	34	16.2	67.5	397	17	US-10-242-535A-33196	Sequence 33196, A
C	35	16.2	67.5	397	18	US-10-085-783A-33196	Sequence 33196, A
C	36	16.2	67.5	408	20	US-10-425-115-112345	Sequence 112345,
	37	16.2	67.5	472	21	US-10-505-680-688	Sequence 688, App
C	38	16.2	67.5	600	21	US-10-956-157-5912	Sequence 5912, Ap
C	39	16.2	67.5	2078	20	US-10-425-115-51743	Sequence 51743, A
C	40	16.2	67.5	2085	20	US-10-739-930-2710	Sequence 2710, Ap
C	41	16.2	67.5	2923	15	US-10-101-510-7	Sequence 7, Appli
C	42	16.2	67.5	2923	17	US-10-366-345-14	Sequence 14, Appl
C	43	16.2	67.5	2923	17	US-10-375-150-7	Sequence 7, Appli
C	44	16.2	67.5	2943	21	US-10-956-157-677	Sequence 677, App
	45	16.2	67.5	3133	17	US-10-291-265-108	Sequence 108, App

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:06:45 ; Search time 189.68 Seconds
                                            (without alignments)
                                            4816.222 Million cell updates/sec

Title: US-10-074-246-48
Perfect score: 24
Sequence: 1 cggccgtccagtcgttaatgtcgc 24

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

| | | % Query | | | | |
Result No.	Score	Match	Length	DB	ID	Description
c 1	19.4	80.8	497	7	CK101783	CK101783 F118P27.5
2	18.2	75.8	452	6	CF026765	CF026765 QCB11f12.
c 3	18.2	75.8	664	9	AG180620	AG180620 Pan trogl
c 4	18.2	75.8	949	9	CNS070DV	AL423497 T7 end of
5	17.8	74.2	987	9	CNS01U2J	AL167284 Tetraodon
c 6	17.8	74.2	1143	9	AG175746	AG175746 Pan trogl
7	17.6	73.3	280	6	CA081232	CA081232 SCACAM204
c 8	17.6	73.3	314	8	BH882141	BH882141 hw35d05.b

c	9	17.6	73.3	383	9	CG229875	CG229875	OGWAK63TH
c	10	17.6	73.3	402	7	CO134696	CO134696	EST829367
c	11	17.6	73.3	424	8	BZ774753	BZ774753	ii49b11.b
c	12	17.6	73.3	428	7	CO137596	CO137596	EST832267
	13	17.6	73.3	457	2	BE516820	BE516820	WHE620_D0
c	14	17.6	73.3	540	4	BJ214160	BJ214160	BJ214160
c	15	17.6	73.3	548	9	CG272919	CG272919	OGWKC66TH
c	16	17.6	73.3	600	8	BZ619480	BZ619480	ig37a07.b
	17	17.6	73.3	600	8	BZ619481	BZ619481	ig37a07.g
c	18	17.6	73.3	613	4	BJ300459	BJ300459	BJ300459
c	19	17.6	73.3	630	4	BJ244447	BJ244447	BJ244447
c	20	17.6	73.3	641	4	BJ256609	BJ256609	BJ256609
c	21	17.6	73.3	650	8	BH819001	BH819001	BACPP12-K
	22	17.6	73.3	656	9	CG824714	CG824714	SOYEB35TH
	23	17.6	73.3	663	7	CN132436	CN132436	OX1_6_D12
	24	17.6	73.3	695	9	CL157668	CL157668	104_345_1
	25	17.6	73.3	762	8	BZ658927	BZ658927	OGCAZ20TC
	26	17.6	73.3	775	7	CN132518	CN132518	OX1_6_D12
	27	17.6	73.3	789	9	CL686083	CL686083	PRI0143a_
	28	17.6	73.3	795	9	CG214781	CG214781	OGXBK26TH
	29	17.6	73.3	801	9	CL666195	CL666195	PRI0151d_
	30	17.6	73.3	850	9	CL654705	CL654705	PRI0121b_
	31	17.6	73.3	852	7	CK416341	CK416341	AUF_IpInt
c	32	17.6	73.3	864	8	BZ658938	BZ658938	OGCAZ20TM
c	33	17.6	73.3	880	6	CD377821	CD377821	PTMM02990
c	34	17.6	73.3	893	6	CD381395	CD381395	PTMM06564
	35	17.4	72.5	894	9	CNS03HB0	AL244053	Tetraodon
c	36	17.2	71.7	505	8	BZ345288	BZ345288	hr48g03.b
	37	17.2	71.7	512	4	BI709947	BI709947	ft51d05.y
c	38	17.2	71.7	513	8	BZ345049	BZ345049	hr44a11.b
	39	17.2	71.7	548	7	CK351188	CK351188	hggfha34D
c	40	17.2	71.7	557	8	AZ396799	AZ396799	1M0161E03
c	41	17.2	71.7	583	7	CO661192	CO661192	DG31-190g
c	42	17.2	71.7	649	1	AI297657	AI297657	LP12009.5
c	43	17.2	71.7	651	1	AI260496	AI260496	LP04383.5
c	44	17.2	71.7	660	7	CR369078	CR369078	CR369078
c	45	17.2	71.7	667	4	BI588806	BI588806	RH30239.5

```
Title:           US-10-074-246-52
Perfect score:   19
Sequence:        1 ccgtccagtcgttaatgtc 19

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:     9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                 1:  gb_ba:*
                 2:  gb_htg:*
                 3:  gb_in:*
                 4:  gb_om:*
                 5:  gb_ov:*
                 6:  gb_pat:*
                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
                 12:  gb_sy:*
                 13:  gb_un:*
                 14:  gb_vi:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	6	AX513123	AX513123 Sequence
2	19	100.0	22	6	BD171663	BD171663 Identific
3	19	100.0	22	6	AX278539	AX278539 Sequence
4	19	100.0	22	6	AX513096	AX513096 Sequence
5	19	100.0	24	6	AX513119	AX513119 Sequence
6	19	100.0	323	6	BD171699	BD171699 Identific
7	19	100.0	369	6	BD171700	BD171700 Identific
8	19	100.0	611	6	BD171688	BD171688 Identific
9	19	100.0	611	6	BD171689	BD171689 Identific
10	19	100.0	628	6	AX513137	AX513137 Sequence
11	19	100.0	802	6	AX513136	AX513136 Sequence
12	19	100.0	110000	1	AE000516_10	Continuation (11 o
13	19	100.0	327650	1	BX248337	BX248337 Mycobacte
14	19	100.0	349306	1	BX842575	BX842575 Mycobacte

C							
c	15	17.4	91.6	214922	2	AC150991	AC150991 Bos tauru
c	16	16.4	86.3	174913	3	AY613856	AY613856 Oikopleur
	17	16	84.2	203592	10	AL669921	AL669921 Mouse DNA
	18	15.8	83.2	620	10	MUSMHW282	M16240 Mouse MHC c
c	19	15.8	83.2	1145	6	AR227484	AR227484 Sequence
	20	15.8	83.2	1362	6	AX078488	AX078488 Sequence
c	21	15.8	83.2	3276	6	A44223	A44223 Sequence 4
c	22	15.8	83.2	3276	6	A72710	A72710 Sequence 4
c	23	15.8	83.2	3276	6	AR408850	AR408850 Sequence
c	24	15.8	83.2	3276	6	AX002862	AX002862 Sequence
c	25	15.8	83.2	3646	1	AY318856	AY318856 Acetobact
	26	15.8	83.2	3849	6	AR385744	AR385744 Sequence
c	27	15.8	83.2	4314	8	GLEY18738	Y18738 Gracilariop
c	28	15.8	83.2	11135	1	AE011096	AE011096 Methanosa
c	29	15.8	83.2	20389	1	AE008768	AE008768 Salmonell
	30	15.8	83.2	70290	2	AC100833	AC100833 Homo sapi
	31	15.8	83.2	71239	2	AC099903	AC099903 Mus muscu
c	32	15.8	83.2	71239	2	AC099903	AC099903 Mus muscu
c	33	15.8	83.2	115857	8	AC147407	AC147407 Medicago
	34	15.8	83.2	144301	9	AC010467	AC010467 Homo sapi
c	35	15.8	83.2	150010	9	AC104782	AC104782 Homo sapi
c	36	15.8	83.2	155164	9	AC005165	AC005165 Homo sapi
c	37	15.8	83.2	155666	10	AC134830	AC134830 Mus muscu
	38	15.8	83.2	155862	9	AC018464	AC018464 Homo sapi
	39	15.8	83.2	159681	10	AC132088	AC132088 Mus muscu
c	40	15.8	83.2	160042	2	AL365211	AL365211 Homo sapi
	41	15.8	83.2	162167	2	AC019271	AC019271 Homo sapi
c	42	15.8	83.2	162167	2	AC019271	AC019271 Homo sapi
c	43	15.8	83.2	169393	9	AC146016	AC146016 Pan trogl
c	44	15.8	83.2	173719	5	BX005313	BX005313 Zebrafish
	45	15.8	83.2	174217	2	AC021408	AC021408 Homo sapi

ALIGNMENTS

GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 07:50:25 ; Search time 22.7553 Seconds
                                            (without alignments)
                                            4942.816 Million cell updates/sec

Title: US-10-074-246-52
Perfect score: 19
Sequence: 1 ccgtccagtcgttaatgtc 19

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004as:*
                13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
      1   19   100.0   19 6   ABS70071   Abs70071 Mycobacte
      2   19   100.0   22 6   ABS70044   Abs70044 Mycobacte
      3   19   100.0   22 6   ABA81861   Aba81861 M tubercu
      4   19   100.0   22 8   ABX10101   Abx10101 M. tuberc
      5   19   100.0   24 6   ABS70067   Abs70067 Mycobacte

	6	19	100.0	628	6	ABS70085	Abs70085 Mycobacte
	7	19	100.0	628	8	ABX10111	Abx10111 M. bovis
	8	19	100.0	648	8	ABX10126	Abx10126 M. tuberc
	9	19	100.0	648	8	ABX10127	Abx10127 M. bovis
	10	19	100.0	802	6	ABS70084	Abs70084 Mycobacte
	11	19	100.0	802	8	ABX10110	Abx10110 M. tuberc
	12	19	100.0	110000	4	AAI99682_10	Continuation (11 o
	13	19	100.0	110000	4	AAI99683_10	Continuation (11 o
C	14	15.8	83.2	417	8	ABZ52746	Abz52746 Aspergill
	15	15.8	83.2	1362	4	AAF60956	Aaf60956 P. putida
C	16	15.8	83.2	3276	2	AAQ88050	Aaq88050 Glucan Ly
C	17	15.8	83.2	3276	2	AAQ87604	Aaq87604 Fungus-in
C	18	15.8	83.2	3276	2	AAV84193	Aav84193 Gracilari
	19	15.8	83.2	3738	8	ACA36064	Aca36064 Prokaryot
	20	15.8	83.2	3849	11	ACH96678	Ach96678 Klebsiell
C	21	15.8	83.2	4316	10	ADB69197	Adb69197 C. neofor
	22	15.8	83.2	229354	6	ABQ74179	Abq74179 Human cyt
	23	15.4	81.1	1157	3	AAF11578	Aaf11578 Aspergill
C	24	15.4	81.1	2383	5	AAS89875	Aas89875 DNA encod
C	25	15.4	81.1	2451	5	AAS85748	Aas85748 DNA encod
	26	15.4	81.1	28136	4	AAK69755	Aak69755 Human imm
	27	15.4	81.1	43011	12	ADN01941	Adn01941 Staphyloc
	28	14.8	77.9	23	12	ADM94964	Adm94964 Herpes si
C	29	14.8	77.9	439	6	ABN96003	Abn96003 Gene #250
	30	14.8	77.9	549	3	AAC95228	Aac95228 Cat flea
C	31	14.8	77.9	617	3	AAF08207	Aaf08207 Fusarium
C	32	14.8	77.9	716	3	AAA54328	Aaa54328 Sequence
C	33	14.8	77.9	725	12	ADQ17340	Adq17340 Human sof
C	34	14.8	77.9	792	12	ADL12782	Adl12782 Human ste
C	35	14.8	77.9	927	2	AAT51317	Aat51317 HSV glyco
	36	14.8	77.9	930	4	AAH33866	Aah33866 Human col
C	37	14.8	77.9	1044	10	ABZ66697	Abz66697 Orthosomy
	38	14.8	77.9	1086	12	ADO48504	Ado48504 Human 108
	39	14.8	77.9	1140	6	ABQ22020	Abq22020 Oligonucl
C	40	14.8	77.9	1140	6	ABQ22021	Abq22021 Oligonucl
C	41	14.8	77.9	1170	13	ADT42664	Adt42664 Bacterial
C	42	14.8	77.9	1180	2	AAZ10960	Aaz10960 HSV-2 gly
C	43	14.8	77.9	1185	2	AAZ10959	Aaz10959 HSV-1 gly
C	44	14.8	77.9	1185	10	ADF12414	Adf12414 Herpes si
C	45	14.8	77.9	1185	12	ADG39432	Adg39432 HSV glyco

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:18:20 ; Search time 6.71004 Seconds
                                           (without alignments)
                                           4633.247 Million cell updates/sec

Title: US-10-074-246-52
Perfect score: 19
Sequence: 1 ccgtccagtcgttaatgtc 19

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
    No.   Score   Match Length DB   ID   Description
    ----
       1   19   100.0 4403765   3 US-09-103-840A-2   Sequence 2, Appli
       2   19   100.0 4411529   3 US-09-103-840A-1   Sequence 1, Appli
c   3   15.8   83.2   1145   3 US-09-221-017B-944   Sequence 944, App
c   4   15.8   83.2   1305   4 US-09-902-540-4277   Sequence 4277, Ap
c   5   15.8   83.2   3276   3 US-08-633-768A-4   Sequence 4, Appli
c   6   15.8   83.2   3276   4 US-09-280-197-4   Sequence 4, Appli
       7   15.8   83.2   3849   4 US-09-489-039A-2473   Sequence 2473, Ap
       8   15.8   83.2   26012   4 US-09-902-540-1212   Sequence 1212, Ap
       9   15.8   83.2   229354   4 US-09-705-400-64   Sequence 64, Appl
c   10   15   78.9   765   4 US-09-248-796A-1849   Sequence 1849, Ap
      11   14.8   77.9   601   4 US-09-949-016-206008   Sequence 206008,

	12	14.8	77.9	601	4	US-09-949-016-206009	Sequence 206009,
c	13	14.8	77.9	792	4	US-09-976-594-511	Sequence 511, App
c	14	14.8	77.9	927	1	US-08-499-568-1	Sequence 1, Appli
c	15	14.8	77.9	927	1	US-08-793-958-1	Sequence 1, Appli
c	16	14.8	77.9	1180	4	US-09-247-890-2	Sequence 2, Appli
c	17	14.8	77.9	1180	4	US-09-724-969-2	Sequence 2, Appli
c	18	14.8	77.9	1180	4	US-09-724-852-2	Sequence 2, Appli
c	19	14.8	77.9	1185	4	US-09-247-890-1	Sequence 1, Appli
c	20	14.8	77.9	1185	4	US-09-724-969-1	Sequence 1, Appli
c	21	14.8	77.9	1185	4	US-09-724-852-1	Sequence 1, Appli
c	22	14.8	77.9	1204	1	US-07-829-947A-1	Sequence 1, Appli
c	23	14.8	77.9	1204	5	PCT-US93-00945-1	Sequence 1, Appli
c	24	14.8	77.9	1242	4	US-09-247-890-3	Sequence 3, Appli
c	25	14.8	77.9	1242	4	US-09-724-969-3	Sequence 3, Appli
c	26	14.8	77.9	1242	4	US-09-724-852-3	Sequence 3, Appli
c	27	14.8	77.9	1459	6	5182195-9	Patent No. 5182195
c	28	14.8	77.9	1459	6	5182195-9	Patent No. 5182195
c	29	14.8	77.9	1550	1	US-08-499-568-10	Sequence 10, Appl
c	30	14.8	77.9	1550	1	US-08-793-958-10	Sequence 10, Appl
c	31	14.8	77.9	1608	1	US-08-499-568-3	Sequence 3, Appli
c	32	14.8	77.9	1608	1	US-08-793-958-3	Sequence 3, Appli
c	33	14.8	77.9	1635	1	US-08-499-568-14	Sequence 14, Appl
c	34	14.8	77.9	1635	1	US-08-793-958-14	Sequence 14, Appl
c	35	14.8	77.9	1635	2	US-08-956-998-1	Sequence 1, Appli
c	36	14.8	77.9	1776	4	US-09-902-540-9057	Sequence 9057, Ap
c	37	14.8	77.9	2643	4	US-09-902-540-2841	Sequence 2841, Ap
	38	14.8	77.9	13299	4	US-09-902-540-968	Sequence 968, App
	39	14.8	77.9	16047	4	US-09-902-540-1136	Sequence 1136, Ap
c	40	14.8	77.9	116966	4	US-09-949-016-17557	Sequence 17557, A
c	41	14.8	77.9	154746	4	US-09-827-688-8	Sequence 8, Appli
c	42	14.4	75.8	364	4	US-09-902-540-2117	Sequence 2117, Ap
c	43	14.4	75.8	428	4	US-09-902-540-1309	Sequence 1309, Ap
c	44	14.4	75.8	711	4	US-09-252-991A-10800	Sequence 10800, A
	45	14.4	75.8	2526	4	US-09-252-991A-10348	Sequence 10348, A

GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 11:13:07 ; Search time 27.6406 Seconds
                                            (without alignments)
                                            4315.680 Million cell updates/sec

Title: US-10-074-246-52
Perfect score: 19
Sequence: 1 ccgtccagtcgttaatgtc 19

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 6330945 seqs, 3139162390 residues

Total number of hits satisfying chosen parameters: 12661890

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                  1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                  2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                  3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                  4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                  5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                  6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                  7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                  8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                  9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                  10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                  11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                  12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                  13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                  14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                  15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                  16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                  17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                  18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                  19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                  20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
                  21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
                  22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                  23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                  24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                  25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                  26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

         Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	19	100.0	19	14	US-10-074-246-52	Sequence 52, Appl
	2	19	100.0	22	9	US-09-817-014-72	Sequence 72, Appl
	3	19	100.0	22	14	US-10-074-246-25	Sequence 25, Appl
	4	19	100.0	22	16	US-10-056-229-72	Sequence 72, Appl
	5	19	100.0	24	14	US-10-074-246-48	Sequence 48, Appl
	6	19	100.0	628	14	US-10-074-246-66	Sequence 66, Appl
	7	19	100.0	802	14	US-10-074-246-65	Sequence 65, Appl
	8	16.4	86.3	743	20	US-10-425-115-173257	Sequence 173257,
C	9	15.8	83.2	1145	13	US-10-194-163-944	Sequence 944, App
C	10	15.8	83.2	3276	9	US-09-280-197-4	Sequence 4, Appli
C	11	15.8	83.2	3276	9	US-09-423-126-8	Sequence 8, Appli
C	12	15.8	83.2	3276	17	US-10-448-139-4	Sequence 4, Appli
C	13	15.8	83.2	3276	21	US-10-879-638-8	Sequence 8, Appli
	14	15.8	83.2	3738	17	US-10-282-122A-23934	Sequence 23934, A
C	15	15.8	83.2	4316	17	US-10-320-797-324	Sequence 324, App
	16	15.8	83.2	218802	21	US-10-897-508-1	Sequence 1, Appli
	17	15.4	81.1	822	18	US-10-424-599-31708	Sequence 31708, A
	18	15.4	81.1	1157	20	US-10-653-047-4101	Sequence 4101, Ap
	19	15.4	81.1	1668	18	US-10-424-599-31707	Sequence 31707, A
	20	14.8	77.9	23	16	US-10-165-410A-16	Sequence 16, Appl
	21	14.8	77.9	25	21	US-10-719-900-182550	Sequence 182550,
C	22	14.8	77.9	263	20	US-10-425-115-165317	Sequence 165317,
	23	14.8	77.9	299	18	US-10-424-599-36371	Sequence 36371, A
C	24	14.8	77.9	439	9	US-09-880-107-2500	Sequence 2500, Ap
C	25	14.8	77.9	495	9	US-09-783-590-4235	Sequence 4235, Ap
	26	14.8	77.9	549	10	US-09-991-936-1723	Sequence 1723, Ap
C	27	14.8	77.9	557	19	US-10-767-701-30650	Sequence 30650, A
C	28	14.8	77.9	617	20	US-10-653-047-730	Sequence 730, App
	29	14.8	77.9	649	13	US-10-027-632-141743	Sequence 141743,
	30	14.8	77.9	649	17	US-10-027-632-141743	Sequence 141743,
C	31	14.8	77.9	725	20	US-10-723-860-157	Sequence 157, App
C	32	14.8	77.9	930	15	US-10-106-698-932	Sequence 932, App
C	33	14.8	77.9	957	18	US-10-425-114-13555	Sequence 13555, A
C	34	14.8	77.9	1041	11	US-09-758-759-12	Sequence 12, Appl
C	35	14.8	77.9	1044	17	US-10-107-431-56	Sequence 56, Appl
C	36	14.8	77.9	1092	19	US-10-669-161-113	Sequence 113, App
	37	14.8	77.9	1140	20	US-10-363-345A-8611	Sequence 8611, Ap
C	38	14.8	77.9	1140	20	US-10-363-345A-8612	Sequence 8612, Ap
	39	14.8	77.9	1140	21	US-10-363-483A-8611	Sequence 8611, Ap
C	40	14.8	77.9	1140	21	US-10-363-483A-8612	Sequence 8612, Ap
C	41	14.8	77.9	1170	17	US-10-369-493-41102	Sequence 41102, A
C	42	14.8	77.9	1180	9	US-09-247-890-2	Sequence 2, Appli
C	43	14.8	77.9	1180	17	US-10-383-317-2	Sequence 2, Appli
C	44	14.8	77.9	1185	9	US-09-247-890-1	Sequence 1, Appli
C	45	14.8	77.9	1185	17	US-10-410-842A-1	Sequence 1, Appli

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 10:06:45 ; Search time 150.164 Seconds
                                          (without alignments)
                                          4816.222 Million cell updates/sec

Title: US-10-074-246-52
Perfect score: 19
Sequence: 1 ccgtccagtcgttaatgtc 19

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                                  SUMMARIES
                       %
Result   Query
    No.   Score   Match Length DB   ID   Description

  C 1   17.4   91.6   497   7   CK101783   CK101783 F118P27.5
  C 2   16.4   86.3   215   4   BG349271   BG349271 947030B12
  C 3   16.4   86.3   363   4   BG349270   BG349270 947030B12
  C 4   16.4   86.3   416   7   CO524986   CO524986 3530_1_16
  C 5   16.4   86.3   431   4   BI273510   BI273510 949026E12
  C 6   16.4   86.3   515   4   BM499183   BM499183 947043D01
  C 7   16.4   86.3   529   4   BG360883   BG360883 947043D01
     8   16.4   86.3   532   4   BI319172   BI319172 949026E12
  C 9   16.4   86.3   552   6   CA141332   CA141332 SCJFRT205
  C 10   16.4   86.3   552   7   CO534599   CO534599 3530_1_22
 ·C 11   16.4   86.3   555   4   BI992275   BI992275 1020058H0
  C 12   16   84.2   754   9   BX958605   BX958605 Forward s
  C 13   16   84.2   883   9   CR055993   CR055993 Forward s

c	14	16	84.2	894	9	BX961662	BX961662	Forward s
c	15	16	84.2	970	9	CR036382	CR036382	Forward s
	16	15.8	83.2	452	6	CF026765	CF026765	QCB11f12.
c	17	15.8	83.2	457	9	CE419457	CE419457	tigr-gss-
c	18	15.8	83.2	650	8	BH819001	BH819001	BACPP12-K
c	19	15.8	83.2	664	9	AG180620	AG180620	Pan trogl
c	20	15.8	83.2	673	7	CO139755	CO139755	EST834426
c	21	15.8	83.2	683	4	BM624199	BM624199	170006874
c	22	15.8	83.2	701	7	CO134722	CO134722	EST829393
c	23	15.8	83.2	725	7	CO687456	CO687456	DG11-231o
	24	15.8	83.2	789	9	CL686083	CL686083	PRI0143a_
	25	15.8	83.2	801	9	CL666195	CL666195	PRI0151d_
c	26	15.8	83.2	847	7	CO144147	CO144147	EST838818
	27	15.8	83.2	850	9	CL654705	CL654705	PRI0121b_
	28	15.8	83.2	1140	4	BG788353	BG788353	SEAUMC008
c	29	15.8	83.2	1143	4	BI763029	BI763029	603047821
c	30	15.8	83.2	1143	9	AG175746	AG175746	Pan trogl
c	31	15.8	83.2	1171	4	BG680034	BG680034	602626775
c	32	15.8	83.2	1350	9	AG398251	AG398251	Mus muscu
	33	15.6	82.1	894	9	CNS03HB0	AL244053	Tetraodon
c	34	15.4	81.1	234	2	BE760944	BE760944	an_0988 A
	35	15.4	81.1	234	8	AQ007681	AQ007681	CIT-HSP-2
c	36	15.4	81.1	284	2	BE760723	BE760723	an_0363 A
	37	15.4	81.1	321	8	BZ762899	BZ762899	SALK_1096
c	38	15.4	81.1	399	8	AQ130249	AQ130249	HS_3007_A
	39	15.4	81.1	404	6	CA914118	CA914118	PCS02012X
c	40	15.4	81.1	417	8	AQ599313	AQ599313	HS_5343_B
	41	15.4	81.1	448	5	BX765912	BX765912	BX765912
c	42	15.4	81.1	472	6	CB278998	CB278998	ru39d09.y
c	43	15.4	81.1	491	4	BM344145	BM344145	rr47c11.y
	44	15.4	81.1	496	5	BU052092	BU052092	gd47f06.y
	45	15.4	81.1	510	9	CL336275	CL336275	RPCI44_25

D-103.

A Prospective Comparison of the MB/BacT™ and Conventional Culturing in a High-Volume Clinical Mycobacteriology Laboratory.

L. STOCKMAN,* D. R. MILLER, and G.D. ROBERTS, Mayo Clinic and Mayo Foundation, Rochester, MN.

During the last decade, with the pressures of managed care, emphasis has been placed on rapid turn-around time, efficient use of technical personnel, and generation of accurate results to aid in patient care. The purpose of this study was to validate the MB/BacT™ instrument and the BacT/View software in a high volume mycobacteriology laboratory. To date, 1105 specimens have been decontaminated and 0.5 mL cultured to BACTEC® 12B Mycobacteria culture vials (BAC), 7H10 and 7H11S (SOL), and MB/BacT™ Process Bottles (MB/B). SOL were read weekly for 8 weeks. BAC were read twice a week for 3 weeks and weekly for 3 weeks, any bottle with a GI =10 was considered positive and aliquots were placed onto a Blood agar (BAP) and into a cytospin AF (Acid fast stain). The MB/B was automatically monitored every 10 min for 6 weeks and positive bottles analyzed by culture (BAP) and smear (AF). All AFB (acid fast bacilli) were identified by probes, biochemicals and/or gas liquid chromatography. Of the 465 cultures completed, 98 cultures were positive and identification of 11 is pending. Isolates recovered include: 50 M. avium intracellulare complex (MAI), 2 M. chelonae (CHEL), 17 M. gordonae (GO) and 16 M. tuberculosis complex (TB). 2 cultures had MAI and CHEL, and MAI and GO, respectively. 57 were positive for AFB in BAC and MB/B. 13 were positive in MB/B only. 6 were positive in BAC only. Of 39 MAI positive in both systems, BAC had an average detection of 7.2 d and range 2-28 d, MB/B had an average 14.5 d and range 2.6-40.7 d. Of the 14 TB positive in both systems, BAC had an average day to detection 9.5 d, and range 8.4-28 d, MB/B had an average 15.8 d, and range 8.5-28.2 d. Due to the instrumentation and BACT/View software, the MB/B was easier to use and required less "hands-on" time. These preliminary results, however, suggest that the MB/B requires a longer incubation time to detection.

D-104.

P34 and F57 Based-Multiplex PCR Assay for Discrimination between Tuberculous and Nontuberculous Mycobacteria.

P. VANNUFFEL, C. COETSIER, M. BOUYER, M. PHILIPPE, J.L. GALA, Queen Astrid Military Hosp. and Univ. of Louvain Medical School, Brussels, Belgium.

The nucleotidic sequences, 5' to the open reading frame encoding the 34 kDa mycobacterial antigenic protein P34, were sequenced in both tuberculous (M. tuberculosis and M. bovis) (MTB) and non-tuberculous (M. avium and M. paratuberculosis) (MAC) mycobacteria. Multiple sequences alignment of this non-transcribed region (5'-NTR) revealed interspecies polymorphisms characterizing both mycobacterial groups : 5'-NTR in MTB species was 79 bases shorter compared to MAC. Conversely, 5'-NTR appeared to be highly conserved within each group : species differenciation relied on a single T to C transition for M. tuberculosis and M. bovis, and a single C to G transversion for M. avium and M. paratuberculosis. In a first sep, a polymerase chain reaction (PCR) assay discriminating MTB from MAC complexes was developped. Primers matching conserved sequences bordering the polymorphic 5'-NTR amplified a 178 bp fragment in MTB and a 257 bp fragment in MCA, irrespective of the species. In a next step, amplification of a 420 bp product from the genomic sequence F57 (1) allowed a specific identification of M. paratuberculosis within the MAC group, and was therefore co-amplified with P34. Based on the P34 and F57 multiplex assay, a distinct amplification pattern was obtained for three of the four mycobacteria: M. paratuberculosis was characterized by the presence of the 420 bp and 257 bp fragments, M. avium by the 257 bp fragment only, while M. tuberculosis and M. bovis indistinctly produced a 178 bp amplicon. Finally, the specificity

of the multiplex assay was confirmed, for the four species, by using a wide panel of reference mycobacteria (n=10), including M. intracellulare, M. africanum, M. microti, M. scrofulaceum, M. kansasii and M. gordonae, and a larger collection of clinical specimens (n=30). While coincidentally also applicable in veterinary medicine, P34 and F57 multiplex assay appears relevant for the detection of human tuberculosis and opportunistic M. avium infections in AIDS patients, and can also be used to assess the putative role of M. paratuberculosis in Crohn's disease or sarcoidosis.

D-105.

Evaluation of the BBL MGIT™ AST SIRE System for Susceptibility Testing of M. tuberculosis.

B.A. HANNA, C.H. REXER, S.B. WALTERS, NYU School of Medicine, Bellevue Hosp. New York, NY.

The global incidence of multidrug-resistant tuberculosis (MDRTB) emphasizes the need for a simple and reliable method for susceptibility testing of Mycobacterium tuberculosis (Mtb). We compared the Mycobacteria Growth Indicator Tube Antimycobacterial Susceptibility Test system (MGIT™AST, Becton Dickinson) to the method of proportion (MOP) disk elution method for the antimycobacterial susceptibility testing of Mtb. The MGIT AST is a four drug rapid susceptibility test system with critical concentrations (µg/ml) of Streptomycin (STR) - 0.8, Isoniazid (INH) - 0.1, Rifampin (RIF) - 1.0 and Ethambutol (EMB) - 3.5, in individual MGIT culture tubes containing modified Middlebrook 7H9 broth and MGIT OADC enrichment along with a growth control tube. For comparison, critical concentrations (ug/ml) tested by MOP were INH - 0.2 and 1.0, RIF - 1.0, STR - 2.0 and 10.0 and EMB - 5.0. For the study, 40 clinical isolates of Mtb including 8 MDRTB, were inoculated to the MGIT AST system and monitored daily for growth. Each isolate was tested in pairs using both a liquid medium (MGIT) and a solid medium (L-J) as the inoculum source. Tubes were read daily, and all growth control tubes were noted to be positive within 3-5 days. Results for drug containing tubes were interpreted when growth was first noted, or within 2 days of the growth control becoming positive. Among the 320 "bug – drug" comparisons there were 5 discordant results. INH: none discordant; RIF: 1 isolate was MGIT R but MOP S in one of the paired tests; STR: 1 isolate was MGIT S but MOP R in one of the paired tests; EMB: 1 isolate was MGIT R but MOP S in one pair, a second isolate was MGIT R but MOP S in both pairs. The MGIT AST is a simple to use, rapid test to detect MDRTB, with excellent comparability to the conventional MOP.

D-106.

rpoB Mutations in Mycobacterium tuberculosis (MTB): an Analysis Using the Polymerase Chain Reaction and Single-Stranded Conformational Polymorphism (PCR-SSCP).

M. BOBADILLA, A. PONCE-DE-LEON*, C. ARENAS, P. COUARY, A. MARTINEZ, G.M. RUIZ-PALACIOS, and J. SIFUENTES-OSORNIO, Inst. Natl. De La Nutricion Salvador Zubiran, Mexico City, Mexico.

Introduction: Resistance to antituberculous agents is an alarming public health problem. A rapid amplification method has been developed that uses SSCP to identify mutations that codify for rifampin (RIF) resistance, which is associated to multi-drug resistance. Objective: To determine mutations in the rpoB gene of MTB clinical isolates with different levels of resistance to RIF using PCR-SSCP analysis. Methods: 45 distinct clinical isolates resistant to at least one antituberculous agent were fully characterized by conventional methods. Minimal inhibitory concentrations (MICs) to RIF were determined by the radiometric method (BACTEC 460, BectonDickinson, Mexico). DNA was extracted using conventional methods. PCR conditions: 10 pM of TB8 (5'TGCACGTCGCGGACCTCCA 3') and TB9 (5'TCGG CGCGATCAAGGAGT 3') primers (codyfing for a 157-bp stretch